STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number 170125

TO: Ruixiang Li **Location: REM/4D75/4C70** **Art Unit: 1646** **Friday, November 25, 2005** **Case Serial Number: 09/475158**	**From: Toby Port** **Location: Biotech-Chem Library** **REM-1A59** **Phone: 571-272-2523** **toby.port@uspto.gov**

Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

STIC-Biotech/ChemLib 170128

From: Li, Ruixiang
Sent: Monday, October 31, 2005 2:39 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.09/475,158

Please do a standard search on:

(i).SEQ ID NOS: 3 and 5 against both commercial and interference amino acid databases;

(ii). SEQ ID NOS: 14, 15, and 16 against both commercial and interference nucleic acid databases;

(iii). AlaValSerGluIleGlnLeuMetHisAsnLeuGlyGlyGlyGlyGly against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 15:52:37 ; Search time 141.5 Seconds
(without alignments)
96.260 Million cell updates/sec

Title: US-09-475-158A-3
Perfect score: 160
Sequence: 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	100.0	31	3	AAY96973	Aay96973 Parathyro
2	146	91.2	31	3	AAY96975	Aay96975 Parathyro
3	133	83.1	38	2	AAR58104	Aar58104 [Gly13]-h
4	129	80.6	34	2	AAR22294	Aar22294 Human par
5	129	80.6	35	2	AAR74462	Aar74462 Parathyro
6	129	80.6	36	2	AAR58271	Aar58271 [Ala11]-h
7	128	80.0	33	3	AAY98015	Aay98015 Human ami
8	128	80.0	34	2	AAW17941	Aaw17941 Human par
9	128	80.0	34	2	AAW67276	Aaw67276 Parathyro
10	128	80.0	34	3	AAY98014	Aay98014 Human ami
11	128	80.0	36	2	AAR58248	Aar58248 N-Dimethy
12	128	80.0	36	2	AAR58026	Aar58026 N-alpha-m
13	128	80.0	36	2	AAR58262	Aar58262 [Ala1]-hP
14	128	80.0	38	2	AAR58019	Aar58019 N-alpha-m
15	127	79.4	31	3	AAY96974	Aay96974 Parathyro
16	127	79.4	34	2	AAR22296	Aar22296 Human par
17	127	79.4	34	2	AAW08117	Aaw08117 Human PTH
18	127	79.4	34	5	AAU73030	Aau73030 Parathyro
19	127	79.4	34	5	AAU73029	Aau73029 Parathyro
20	127	79.4	34	8	ADQ75344	Adq75344 PTH/PTHrP
21	127	79.4	34	8	ADQ75345	Adq75345 PTH/PTHrP
22	127	79.4	35	2	AAR74466	Aar74466 Parathyro
23	127	79.4	35	2	AAR74470	Aar74470 Parathyro
24	127	79.4	35	5	AAU73173	Aau73173 Parathyro
25	127	79.4	35	8	ADQ75490	Adq75490 PTH/PTHrP
26	127	79.4	35	8	ADQ75489	Adq75489 PTH/PTHrP
27	127	79.4	36	2	AAR58209	Aar58209 [Ala14]-h
28	127	79.4	36	2	AAR58207	Aar58207 [Ala13]-h
29	127	79.4	38	2	AAR58024	Aar58024 [Ala1,Ile
30	127	79.4	38	2	AAR58037	Aar58037 [Ser14]-h
31	127	79.4	38	2	AAR58093	Aar58093 [Asn13]-h
32	127	79.4	38	2	AAR58098	Aar58098 [Ser13]-h
33	127	79.4	38	2	AAR58103	Aar58103 [Ala13]-h
34	127	79.4	38	2	AAR58106	Aar58106 [Ala14]-h
35	126	78.8	31	9	ADW95207	Adw95207 Amino aci
36	126	78.8	31	9	ADW95208	Adw95208 Amino aci
37	126	78.8	34	2	AAR22292	Aar22292 Human par
38	126	78.8	34	2	AAW08108	Aaw08108 Human par
39	126	78.8	38	2	AAR58095	Aar58095 [Asp13]-h
40	125	78.1	31	2	AAW42059	Aaw42059 Human par
41	125	78.1	31	2	AAW42051	Aaw42051 Human par
42	125	78.1	31	2	AAY02578	Aay02578 N-termina
43	125	78.1	31	4	AAB81080	Aab81080 Human par
44	125	78.1	31	4	AAB91097	Aab91097 Parathyro
45	125	78.1	31	5	AAE23720	Aae23720 Human par

ALIGNMENTS

RESULT 1
AAY96973
ID AAY96973 standard; peptide; 31 AA.
XX
AC AAY96973;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone functional domain conjugate peptide PG5.
XX
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .9
FT /label= PTH_N-terminal_signaling_domain
FT /note= "residues 1-9"
FT Peptide 10. .14
FT /label= linker
FT Peptide 15. .30
FT /label= PTH_C-terminal_binding_portion
FT /note= "residues 15-31"
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
DR N-PSDB; AAA51729.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.

```
XX
PS   Claim 7; Page 92-93; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 31 AA;

  Query Match             100.0%;  Score 160;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-14;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||||||||||||||||||||||||
Db          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31


RESULT 2
AAY96975
ID   AAY96975 standard; peptide; 31 AA.
XX
AC   AAY96975;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Parathyroid hormone functional domain conjugate peptide PG7.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .9
FT                   /label= PTH_N-terminal_signaling_domain
FT                   /note= "residues 1-9"
FT   Peptide         10. .16
FT                   /label= linker
FT   Peptide         17. .31
FT                   /label= PTH_C-terminal_binding_portion
FT                   /note= "residues 17-31"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   N-PSDB; AAA51730.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 7; Page 93; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 31 AA;

  Query Match             91.2%;  Score 146;  DB 3;  Length 31;
  Best Local Similarity   93.5%;  Pred. No. 1.2e-12;
  Matches   29;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||||||  ||||||||||||||
Db          1 AVSEIQLMHGGGGGGGSMERVEWLRKKLQDV 31


RESULT 3
AAR58104
ID   AAR58104 standard; peptide; 38 AA.
XX
AC   AAR58104;
XX
DT   20-SEP-1994  (first entry)
XX
DE   [Gly13]-hPTH(1-38)-OH.
XX
KW   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
KW   fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX
OS   Synthetic.
XX
PN   GB2269176-A.
XX
PD   02-FEB-1994.
XX
PF   12-JUL-1993;   93GB-00014384.
XX
PR   15-JUL-1992;   92GB-00015009.
PR   18-DEC-1992;   92GB-00026415.
PR   23-DEC-1992;   92GB-00026859.
PR   23-DEC-1992;   92GB-00026861.
PR   28-JAN-1993;   93GB-00001691.
PR   28-JAN-1993;   93GB-00001692.
PR   14-APR-1993;   93GB-00007673.
PR   19-APR-1993;   93GB-00008033.
XX
PA   (SANO ) SANDOZ LTD.
XX
PI   Lewis I,  Schneider H,  Waelchli R,  Rainer A;
XX
DR   WPI; 1994-018352/03.
XX
PT   New active para-thyroid hormone variants - used for treating or
PT   preventing osteoporosis etc.
XX
PS   Example 101; Page 39; 92pp; English.
XX
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CC   This peptide is an example of a highly generic formula covering
CC   parathyroid hormone variants useful for treating or preventing bone
CC   conditions associated with calcium depletion/resorption, in cases where
CC   calcium fixation is required (esp. osteoporosis) or to treat
CC   hypoparathyroidism
XX
SQ   Sequence 38 AA;

  Query Match             83.1%;  Score 133;  DB 2;  Length 38;
  Best Local Similarity   87.1%;  Pred. No. 9e-11;
  Matches   27;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||||||||  || ||||||||||||||||
Db          1 SVSEIQLMHNLGGHLNSMERVEWLRKKLQDV 31


RESULT 4
AAR22294
ID   AAR22294 standard; peptide; 34 AA.
XX
AC   AAR22294;
XX
DT   25-MAR-2003  (revised)
DT   03-AUG-1992  (first entry)
XX
DE   Human parathyroid hormone 1-34 [Ser 11].
XX
KW   hPTH; protease resistant; osteoporosis; hypoparathyroidism; hypertension.
XX
OS   Synthetic.
XX
PN   EP477885-A.
XX
PD   01-APR-1992.
XX
PF   25-SEP-1991;   91EP-00116303.
XX
PR   28-SEP-1990;   90JP-00257490.
PR   06-SEP-1991;   91JP-00227232.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Nakagawa S,  Fukuda T,  Kawase M,  Yamazaki I;
XX
DR   WPI; 1992-106285/14.
XX
PT   New peptide(s) are parathyroid hormone derivs. - used in hormone therapy,
PT   for treating osteoporosis hyperparathyroidism and hypertension.
XX
PS   Claim 9; Page 14; 14pp; English.
XX
CC   The peptide is an analogue of human parathyroid hormone fragment 1-34.
CC   The peptide modification defined increase resistance to proteases and
CC   therefore persistance in the blood. The peptide is used in therapy of
CC   osteoporosis, hypoparathyroidism and hypertension. The peptide may be
CC   synthesised by the Merrifield solid phase method in an automatic
CC   apparatus. See also AAR22290-99. (Updated on 25-MAR-2003 to correct PA
CC   field.)
XX
SQ   Sequence 34 AA;

  Query Match             80.6%;  Score 129;  DB 2;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-10;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||||||||  |  ||||||||||||||||
Db          1 SVSEIQLMHNSGKHLNSMERVEWLRKKLQDV 31


RESULT 5
AAR74462
ID   AAR74462 standard; peptide; 35 AA.
XX
AC   AAR74462;
XX
DT   25-MAR-2003  (revised)
DT   01-DEC-1995  (first entry)
XX
DE   Parathyroid hormone peptide analogue, Gly11.
XX
KW   Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
KW   osteoporosis; hypercalcaemia; hyperparathroidism; metabolic bone disease;
KW   human; veterinary medicine; iontophoretic transdermal transport;
KW   recombinant E.coli.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   35
FT                   /label= -H, OTHER
FT                   /note= "Homoserine (Hse), Hse lactone, Hse amide or
FT                   residues 35-84 of PTH"
XX
PN   WO9511988-A1.
XX
PD   04-MAY-1995.
XX
PF   25-OCT-1994;   94WO-US012205.
XX
PR   25-OCT-1993;   93US-00142551.
XX
PA   (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI   Oldenburg KR,  Selick HE;
XX
DR   WPI; 1995-178880/23.
XX
PT   New active analogues of parathyroid hormone - with increased activity,
PT   stability in serum etc., esp. for treating osteoporosis, also related DNA
PT   and vectors.
XX
PS   Example 4; Page 76; 109pp; English.
XX
CC   The sequences given in AAR74429-520 represent analogues of the 34 amino
CC   acid sequence of truncated human parathyroid hormone (PTH). These
CC   analogues have increased activity and longer serum half life than native
CC   PTH due to eg. substitution of Met residues with Leu residues and
CC   replacing the carboxy Phe with Tyr. The carboxy terminal may also be
CC   modified by the addition of a homoserine residue or analogue, or by the
CC   addition of residues 35-84 of wild type PTH (see AAR74410). These PTH
CC   analogues may be used in the treatment of osteoporosis or hypercalcaemia,
CC   hyperparathroidism or other metabolic bone diseases in human or
CC   veterinary medicine. These peptides may also have increased iontophoretic
CC   transdermal transport compared to wild type PTH and can be produced in
CC   high yield in recombinant E.coli. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 35 AA;

  Query Match             80.6%;  Score 129;  DB 2;  Length 35;
  Best Local Similarity   80.6%;  Pred. No. 2.9e-10;
  Matches   25;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||:| ||  |||:||||||||||||
Db          1 SVSEIQLLHNGGKHLNSLERVEWLRKKLQDV 31


RESULT 6
AAR58271
ID   AAR58271 standard; peptide; 36 AA.
XX
AC   AAR58271;
XX
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```
DT   20-SEP-1994  (first entry)
XX
DE   [Ala11]-hPTH(1-36)-NH2.
XX
KW   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
KW   fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   36
FT                   /note= "in amide form"
XX
PN   GB2269176-A.
XX
PD   02-FEB-1994.
XX
PF   12-JUL-1993;   93GB-00014384.
XX
PR   15-JUL-1992;   92GB-00015009.
PR   18-DEC-1992;   92GB-00026415.
PR   23-DEC-1992;   92GB-00026859.
PR   23-DEC-1992;   92GB-00026861.
PR   28-JAN-1993;   93GB-00001691.
PR   28-JAN-1993;   93GB-00001692.
PR   14-APR-1993;   93GB-00007673.
PR   19-APR-1993;   93GB-00008033.
XX
PA   (SANO ) SANDOZ LTD.
XX
PI   Lewis I,  Schneider H,  Waelchli R,  Rainer A;
XX
DR   WPI; 1994-018352/03.
XX
PT   New active para-thyroid hormone variants - used for treating or
PT   preventing osteoporosis etc.
XX
PS   Example 269; Page 46; 92pp; English.
XX
CC   This peptide is an example of a highly generic formula covering
CC   parathyroid hormone variants useful for treating or preventing bone
CC   conditions associated with calcium depletion/resorption, in cases where
CC   calcium fixation is required (esp. osteoporosis) or to treat
CC   hypoparathyroidism
XX
SQ   Sequence 36 AA;

  Query Match             80.6%;  Score 129;  DB 2;  Length 36;
  Best Local Similarity   83.9%;  Pred. No. 3e-10;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||||
Db          1 SVSEIQLMHNAGKHLNSMERVEWLRKKLQDV 31


RESULT 7
AAY98015
ID   AAY98015 standard; peptide; 33 AA.
XX
AC   AAY98015;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Human amino-terminal modified parathyroid hormone analogue # 6.
XX
KW   Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;
KW   signal transduction; osteoporosis; amino-terminal modification;
KW   bone disease; parathyroid hormone receptor; osteopaenia;
KW   hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Ala is desamino residue"
XX
PN   WO200031137-A1.
XX
PD   02-JUN-2000.
XX
PF   23-NOV-1999;   99WO-US027656.
XX
PR   25-NOV-1998;   98US-0110152P.
XX
PA   (BRIN/) BRINGHURST F R.
PA   (TAKA/) TAKASU H.
PA   (GARD/) GARDELLA T J.
XX
PI   Bringhurst FR,  Takasu H,  Gardella TJ;
XX
DR   WPI; 2000-400045/34.
XX
PT   New parathyroid hormone (PTH) analogs having one or more amino acid
PT   substitutions that confer PTH-1/PTH-2 receptor agonist properties, useful
PT   for treating old age osteoporosis and post-menopausal osteoporosis.
XX
PS   Disclosure; Page 64; 69pp; English.
XX
CC   Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC   cells, initiating signal transduction. It has been identified that the
CC   carboxyl terminal of PTH is important for PTH receptor binding, while the
CC   amino terminal is important for signal transduction. The present sequence
CC   is a human PTH peptide, with an amino-terminal modification which results
CC   in effective activation of the PTH-2 receptor and therefore downstream
CC   signalling. Aberrant PTH activity has been implicated in a number of
CC   disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC   hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC   and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC   myeloma and epidermoid cancers of the head, neck and oesophagus. This
CC   peptide would be suitable for prophylaxis and treatment of the above
CC   disorders. In addition, the present sequence would be suitable for
CC   fracture repair. The present sequence is modified to have a desamino
CC   residue at position 1
XX
SQ   Sequence 33 AA;

  Query Match             80.0%;  Score 128;  DB 3;  Length 33;
  Best Local Similarity   87.1%;  Pred. No. 3.8e-10;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||| |  ||||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 8
AAW17941
ID   AAW17941 standard; peptide; 34 AA.
XX
AC   AAW17941;
XX
DT   29-JUL-1997  (first entry)
XX
DE   Human parathyroid hormone analogue [Cha11]hPTH(1-34)NH2.
XX
KW   Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW   bone fracture.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   11
FT                   /label= OTHER
FT                   /note= "Cyclohexylalanine (Cha)"
```

```
FT   Modified-site   34
FT                   /note= "In amide form"
XX
PN   WO9702834-A1.
XX
PD   30-JAN-1997.
XX
PF   03-JUL-1996;    96WO-US011292.
XX
PR   13-JUL-1995;    95US-0001105P.
PR   06-SEP-1995;    95US-0003305P.
PR   29-MAR-1996;    96US-00626186.
XX
PA   (BIOM-) BIOMEASURE INC.
XX
PI   Dong ZX;
XX
DR   WPI; 1997-118819/11.
XX
PT   New variants of human parathyroid hormone 1-34 peptide - which stimulate
PT   bone growth and are used for treatment of osteoporosis and bone fracture.
XX
PS   Claim 5; Page; 33pp; English.
XX
CC   The present sequence is a specific example of a human parathyroid hormone
CC   (hPTH) analogue from fragment 1-34 in which at least one of the amino
CC   acid residues at positions 7, 11, 23, 24, 27, 28 and 31 is
CC   cyclohexylalanine (Cha). In this example the Leu residue at position 11
CC   of the wild-type has been substituted by Cha. The hPTH analogues
CC   stimulate bone growth and so are useful in human or veterinary medicine
CC   for treatment of osteoporosis and bone fracture, optionally in
CC   conjunction with anti-resorptive therapy (bisphosphonates and
CC   calcitonin). N.B. The present sequence does not appear in the
CC   specification. It corresponds to the known hPTH 1-34 fragment with the
CC   modifications as stated in the claim
XX
SQ   Sequence 34 AA;

  Query Match             80.0%;  Score 128;  DB 2;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 3.9e-10;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||||||||  |  ||||||||||||||||
Db          1 SVSEIQLMHNXGKHLNSMERVEWLRKKLQDV 31


RESULT 9
AAW67276
ID   AAW67276 standard; peptide; 34 AA.
XX
AC   AAW67276;
XX
DT   22-DEC-1998  (first entry)
XX
DE   Parathyroid hormone analogue #3.
XX
KW   Parathyroid hormone; parathormone; bone growth; bone fracture;
KW   osteroporosis; anti-resorptive therapy; calcitonin.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   11
FT                   /note= "1-amino-1-cyclohexanecarboxylic acid"
FT   Modified-site   34
FT                   /note= "C-terminal amide"
XX
PN   WO9830590-A2.
XX
PD   16-JUL-1998.
XX
PF   08-DEC-1997;    97WO-US022498.
XX
PR   07-JAN-1997;    97US-00779768.
PR   07-MAR-1997;    97US-00813534.
XX
PA   (BIOM-) BIOMEASURE INC.
XX
PI   Dong ZX;
XX
DR   WPI; 1998-399065/34.
XX
PT   Parathyroid hormone analogue peptide compounds - used for stimulating
PT   bone growth, e.g. in treatment of bone fractures or osteoporosis.
XX
PS   Claim 6; Page; 24pp; English.
XX
CC   The invention relates to peptides of formula (I) containing at least one
CC   Acc (i.e. 1-amino-1-(3-9C cycloalkane)-carboxylic acid) residue.
CC   (R1)(R2)A1-Val-A3-Glu-A5-Gln-A7-A8-His-Asn-A11-A12-Lys-His-A15-A-16-A17-
CC   A-18-A19-Arg-A21-A22-A23-A24-Arg-Lys-A27-A28-A29-A30-A31-A32-A33-A34-R3
CC   (I); where A1 = Ser, Ala or Dap; A3, A17 = Ser, Thr or Aib; A5, A7, A11,
CC   A15 = Leu, Nle, Ile, Cha, beta -Nal, Trp, Pal, Acc, Phe or p-(X)-Phe; X =
CC   OH, halo or Me; A8 = Met, Nva, Leu, Val, Ile, Cha, Acc or Nle; A12 = Gly,
CC   Acc or Aib; A16 = Ser, Asn, Ala or Aib; A18 = Met, Nva, Leu, Val, Ile,
CC   Nle, Acc, Cha or Aib; A19 = Glu or Aib; A21 = Val, Acc, Cha or Met; A22 =
CC   Acc or Glu; A'23 = Trp, Acc or Cha; A24, A28 = Leu, Acc or Cha; A27 =
CC   Lys, Aib, Leu, hArg, Gln, Acc or Cha; A29 = Glu, Acc or Aib; A30 = Asp or
CC   Lys; A31 = Val, Leu, Nle, Acc or Cha, or is deleted; A32 = His or is
CC   deleted; A33 = Asn or is deleted; A34 = Phe, Tyr, Amp or Aib, or is
CC   deleted; R1,R2 = H, 1-12C alkyl, 2-12C alkenyl, 7-20C phenylalkyl, 11-20C
CC   naphthylalkyl, 1-12C hydroxyalkyl, 2-12C hydroxyalkenyl, 7-20C
CC   hydroxyphenylalkyl or 11-20C hydroxy-naphthylalkyl; one of R1 and R2 may
CC   also = COE; E = 1-12C alkyl, 2-12C alkenyl, 7-20C phenylalkyl, 11-20C
CC   naphthylalkyl, 1-12C hydroxyalkyl, 2-12C hydroxyalkenyl, 7-20C
CC   hydroxyphenylalkyl or 11-20C hydroxy-naphthylalkyl; R3 = OH, NH2, 1-12C
CC   alkoxy or -NH-Y-CH2-Z; Y = 1-12C hydrocarbyl; Z = H, OH, COOH or CONH2.
CC   The peptides are variants of fragments of parathyroid hormone (PTH) or
CC   parathyroid hormone-related protein (PTHrP). They stimulate bone growth,
CC   and are useful in the treatment of diseases or disorders associated with
CC   bone growth deficiency, e.g. osteoporosis and bone fractures. They are
CC   optionally used in conjunction with anti-resorptive therapy, e.g. with
CC   bis-phosphonates or calcitonin. The present sequence represents a
CC   specifically claimed peptide. NB: This sequence is not shown explicitly
CC   in the patent but was generated using the sequence of human parathyroid
CC   hormone as shown in Entrez Locus Number AAA29146
XX
SQ   Sequence 34 AA;

  Query Match             80.0%;  Score 128;  DB 2;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 3.9e-10;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||||||||  |  ||||||||||||||||
Db          1 SVSEIQLMHNXGKHLNSMERVEWLRKKLQDV 31


RESULT 10
AAY98014
ID   AAY98014 standard; peptide; 34 AA.
XX
AC   AAY98014;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Human amino-terminal modified parathyroid hormone analogue # 5.
XX
KW   Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;
KW   signal transduction; osteoporosis; amino-terminal modification;
KW   bone disease; parathyroid hormone receptor; osteopaenia;
KW   hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Ala is desamino residue"
XX
PN   WO200031137-A1.
XX
PD   02-JUN-2000.
XX
PF   23-NOV-1999;   99WO-US027656.
XX
PR   25-NOV-1998;   98US-0110152P.
XX
PA   (BRIN/) BRINGHURST F R.
PA   (TAKA/) TAKASU H.
PA   (GARD/) GARDELLA T J.
XX
PI   Bringhurst FR,  Takasu H,  Gardella TJ;
XX
DR   WPI; 2000-400045/34.
XX
PT   New parathyroid hormone (PTH) analogs having one or more amino acid
PT   substitutions that confer PTH-1/PTH-2 receptor agonist properties, useful
PT   for treating old age osteoporosis and post-menopausal osteoporosis.
XX
PS   Claim 3; Page 63; 69pp; English.
XX
CC   Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC   cells, initiating signal transduction. It has been identified that the
CC   carboxyl terminal of PTH is important for PTH receptor binding, while the
CC   amino terminal is important for signal transduction. The present sequence
CC   is a human PTH peptide, with an amino-terminal modification which results
CC   in effective activation of the PTH-2 receptor and therefore downstream
CC   signalling. Aberrant PTH activity has been implicated in a number of
CC   disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC   hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC   and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC   myeloma and epidermoid cancers of the head, neck and oesophagus. This
CC   peptide would be suitable for prophylaxis and treatment of the above
CC   disorders. In addition, the present sequence would be suitable for
CC   fracture repair. The present sequence is modified to have a desamino
CC   residue at position 1
XX
SQ   Sequence 34 AA;

  Query Match             80.0%;  Score 128;  DB 3;  Length 34;
  Best Local Similarity   87.1%;  Pred. No. 3.9e-10;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 11
AAR58248
ID   AAR58248 standard; peptide; 36 AA.
XX
AC   AAR58248;
XX
DT   20-SEP-1994  (first entry)
XX
DE   N-Dimethyl-[Ala1]-hPTH(1-36)-NH2.
XX
KW   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
KW   fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /label= Other
FT                   /note= "N-Dimethyl-Ala."
FT   Modified-site   36
FT                   /note= "in amide form"
XX
PN   GB2269176-A.
XX
PD   02-FEB-1994.
XX
PF   12-JUL-1993;   93GB-00014384.
XX
PR   15-JUL-1992;   92GB-00015009.
PR   18-DEC-1992;   92GB-00026415.
PR   23-DEC-1992;   92GB-00026859.
PR   23-DEC-1992;   92GB-00026861.
PR   28-JAN-1993;   93GB-00001691.
PR   28-JAN-1993;   93GB-00001692.
PR   14-APR-1993;   93GB-00007673.
PR   19-APR-1993;   93GB-00008033.
XX
PA   (SANO ) SANDOZ LTD.
XX
PI   Lewis I,  Schneider H,  Waelchli R,  Rainer A;
XX
DR   WPI; 1994-018352/03.
XX
PT   New active para-thyroid hormone variants - used for treating or
PT   preventing osteoporosis etc.
XX
PS   Example 244; Page 45; 92pp; English.
XX
CC   This peptide is an example of a highly generic formula covering
CC   parathyroid hormone variants useful for treating or preventing bone
CC   conditions associated with calcium depletion/resorption, in cases where
CC   calcium fixation is required (esp. osteoporosis) or to treat
CC   hypoparathyroidism
XX
SQ   Sequence 36 AA;

  Query Match             80.0%;  Score 128;  DB 2;  Length 36;
  Best Local Similarity   87.1%;  Pred. No. 4.1e-10;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 12
AAR58026
ID   AAR58026 standard; peptide; 36 AA.
XX
AC   AAR58026;
XX
DT   20-SEP-1994  (first entry)
XX
DE   N-alpha-methyl[Ala1] parathyroid hormone(1-36).
XX
KW   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
KW   fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-alpha-methyl-Ala replaces wild-type Ser residue
FT                   at position 1"
XX
PN   GB2269176-A.
XX
PD   02-FEB-1994.
XX
PF   12-JUL-1993;   93GB-00014384.
XX
PR   15-JUL-1992;   92GB-00015009.
```

```
PR   18-DEC-1992;   92GB-00026415.
PR   23-DEC-1992;   92GB-00026859.
PR   23-DEC-1992;   92GB-00026861.
PR   28-JAN-1993;   93GB-00001691.
PR   28-JAN-1993;   93GB-00001692.
PR   14-APR-1993;   93GB-00007673.
PR   19-APR-1993;   93GB-00008033.
XX
PA   (SANO ) SANDOZ LTD.
XX
PI   Lewis I,  Schneider H,  Waelchli R,  Rainer A;
XX
DR   WPI; 1994-018352/03.
XX
PT   New active para-thyroid hormone variants - used for treating or
PT   preventing osteoporosis etc.
XX
PS   Example 12; Page 35; 92pp; English.
XX
CC   This peptide is an example of a highly generic formula covering
CC   parathyroid hormone variants useful for treating or preventing bone
CC   conditions associated with calcium depletion/resorption, in cases where
CC   calcium fixation is required (esp. osteoporosis) or to treat
CC   hypoparathyroidism
XX
SQ   Sequence 36 AA;

  Query Match             80.0%;  Score 128;  DB 2;  Length 36;
  Best Local Similarity   87.1%;  Pred. No. 4.1e-10;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 13
AAR58262
ID   AAR58262 standard; peptide; 36 AA.
XX
AC   AAR58262;
XX
DT   20-SEP-1994  (first entry)
XX
DE   [Ala1]-hPTH(1-36)-NH2.
XX
KW   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
KW   fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   36
FT                   /note= "in amide form"
XX
PN   GB2269176-A.
XX
PD   02-FEB-1994.
XX
PF   12-JUL-1993;   93GB-00014384.
XX
PR   15-JUL-1992;   92GB-00015009.
PR   18-DEC-1992;   92GB-00026415.
PR   23-DEC-1992;   92GB-00026859.
PR   23-DEC-1992;   92GB-00026861.
PR   28-JAN-1993;   93GB-00001691.
PR   28-JAN-1993;   93GB-00001692.
PR   14-APR-1993;   93GB-00007673.
PR   19-APR-1993;   93GB-00008033.
XX
PA   (SANO ) SANDOZ LTD.
XX
PI   Lewis I,  Schneider H,  Waelchli R,  Rainer A;
XX
DR   WPI; 1994-018352/03.
XX
PT   New active para-thyroid hormone variants - used for treating or
PT   preventing osteoporosis etc.
XX
PS   Example 260; Page 46; 92pp; English.
XX
CC   This peptide is an example of a highly generic formula covering
CC   parathyroid hormone variants useful for treating or preventing bone
CC   conditions associated with calcium depletion/resorption, in cases where
CC   calcium fixation is required (esp. osteoporosis) or to treat
CC   hypoparathyroidism
XX
SQ   Sequence 36 AA;

  Query Match             80.0%;  Score 128;  DB 2;  Length 36;
  Best Local Similarity   87.1%;  Pred. No. 4.1e-10;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 14
AAR58019
ID   AAR58019 standard; peptide; 38 AA.
XX
AC   AAR58019;
XX
DT   20-SEP-1994  (first entry)
XX
DE   N-alpha-methyl[Ala1] parathyroid hormone(1-38).
XX
KW   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
KW   fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-alpha-methyl-Ala replaces wild-type Ser residue
FT                   at position 1"
XX
PN   GB2269176-A.
XX
PD   02-FEB-1994.
XX
PF   12-JUL-1993;   93GB-00014384.
XX
PR   15-JUL-1992;   92GB-00015009.
PR   18-DEC-1992;   92GB-00026415.
PR   23-DEC-1992;   92GB-00026859.
PR   23-DEC-1992;   92GB-00026861.
PR   28-JAN-1993;   93GB-00001691.
PR   28-JAN-1993;   93GB-00001692.
PR   14-APR-1993;   93GB-00007673.
PR   19-APR-1993;   93GB-00008033.
XX
PA   (SANO ) SANDOZ LTD.
XX
PI   Lewis I,  Schneider H,  Waelchli R,  Rainer A;
XX
DR   WPI; 1994-018352/03.
XX
PT   New active para-thyroid hormone variants - used for treating or
PT   preventing osteoporosis etc.
XX
PS   Example 4; Page 34; 92pp; English.
XX
CC   This peptide is an example of a highly generic formula covering
CC   parathyroid hormone variants useful for treating or preventing bone
```

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CC   conditions associated with calcium depletion/resorption, in cases where
CC   calcium fixation is required (esp. osteoporosis) or to treat
CC   hypoparathyroidism
XX
SQ   Sequence 38 AA;

  Query Match             80.0%;  Score 128;  DB 2;  Length 38;
  Best Local Similarity   87.1%;  Pred. No. 4.4e-10;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 15
AAY96974
ID   AAY96974 standard; peptide; 31 AA.
XX
AC   AAY96974;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Parathyroid hormone functional domain conjugate peptide PG9.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .5
FT                   /label= PTH_N-terminal_signaling_domain
FT                   /note= "residues 1-5"
FT   Peptide         6. .14
FT                   /label= linker
FT   Peptide         15. .31
FT                   /label= PTH_C-terminal_binding_portion
FT                   /note= "residues 15-31"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   N-PSDB; AAA51731.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 7; Page 93; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 31 AA;

  Query Match             79.4%;  Score 127;  DB 3;  Length 31;
  Best Local Similarity   87.1%;  Pred. No. 4.8e-10;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||    ||||||||||||||||||||||
Db          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31


Search completed: November 21, 2005, 16:10:11
Job time : 142.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:05:13 ; Search time 23.5 Seconds
(without alignments)
126.924 Million cell updates/sec

Title: US-09-475-158A-3
Perfect score: 160
Sequence: 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	125	78.1	115	1	PTHU	parathyroid hormon
2	119	74.4	115	1	PTBO	parathyroid hormon
3	117	73.1	115	1	PTPG	parathyroid hormon
4	116	72.5	115	2	JC4202	parathyroid hormon
5	110	68.8	115	2	A05091	parathyroid hormon
6	105	65.6	105	2	I51851	parathyroid hormon
7	85	53.1	119	2	A34937	parathyroid hormon
8	62	38.8	641	2	B43777	choline O-acetyltr
9	62	38.8	644	2	A48319	choline O-acetyltr
10	60	37.5	626	2	A55720	carnitine O-acetyl
11	59	36.9	990	2	T03784	probable receptor
12	57	35.6	110	2	D69651	PTS lichenan-speci
13	56	35.0	399	1	HMXRH2	sigma 1 protein -
14	56	35.0	462	2	C34829	sigma 1 protein -
15	56	35.0	627	2	S52782	carnitine acetyltr
16	56	35.0	641	2	A39961	choline O-acetyltr
17	56	35.0	748	2	A60202	choline O-acetyltr
18	55	34.4	463	1	S74845	tldD homolog slr08
19	55	34.4	614	2	T18745	hypothetical prote
20	54	33.8	627	2	S53369	carnitine O-acetyl
21	53	33.1	534	2	S62572	hypothetical prote
22	52	32.5	225	2	S67772	hypothetical prote
23	52	32.5	786	2	A53939	kinesin homolog KH
24	51.5	32.2	421	2	T10190	L-ascorbate peroxi
25	51	31.9	258	2	I39767	acetylglutamate ki
26	51	31.9	588	2	T45539	moaD protein [impo
27	50.5	31.6	319	2	T45980	hypothetical prote
28	50.5	31.6	1375	2	F82336	DNA-directed RNA p
29	50	31.2	443	1	BVBYR1	mevalonate kinase
30	50	31.2	1257	1	I58383	retinoblastoma bin
31	50	31.2	1922	2	T00637	hypothetical prote
32	49.5	30.9	158	2	H83405	hypothetical prote
33	49.5	30.9	275	2	E95231	pur operon repress
34	49.5	30.9	275	2	G98095	activator of purin
35	49	30.6	325	2	E72421	acetyl xylan ester
36	49	30.6	425	2	T03605	probable DNA bindi
37	49	30.6	720	2	A36526	choline O-acetyltr
38	49	30.6	728	2	A24889	choline O-acetyltr
39	48.5	30.3	219	2	T45997	hypothetical prote
40	48	30.0	94	2	T09450	virulence-associat
41	48	30.0	94	2	C64559	virulence associat
42	48	30.0	176	1	S10202	parathyroid hormon
43	48	30.0	301	2	G72698	hypothetical prote
44	48	30.0	361	1	A64221	MgPa operon hypoth
45	48	30.0	506	2	C42725	amidase (EC 3.5.1.

ALIGNMENTS

RESULT 1
PTHU
parathyroid hormone precursor [validated] - human
N;Alternate names: proparathyroid hormone
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410; I38
R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
A;Title: Nucleotide sequence of the human parathyroid hormone gene.
A;Reference number: A19339; MUID:83169834; PMID:6220408
A;Accession: A19339
A;Molecule type: DNA
A;Residues: 1-115 <VAS>
A;Cross-references: UNIPROT:P01270; UNIPARC:UPI000013290A; GB:J00301; NID:g190702; PIDN:
R;Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.
Biol. Chem. Hoppe-Seyler 375, 821-824, 1994
A;Title: Purification of meprin from human kidney and its role in parathyroid hormone de
A;Reference number: S53790; MUID:95225988; PMID:7710697
A;Accession: S53790
A;Molecule type: protein
A;Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>
A;Cross-references: UNIPARC:UPI00001734E1; UNIPARC:UPI00001734E2; UNIPARC:UPI00001734E3
A;Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occurre
R;Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974
A;Title: Structural analysis of human proparathyroid hormone by a new microsequencing ap
A;Reference number: A93169; MUID:74174967; PMID:4833516
A;Accession: A93169
A;Molecule type: protein
A;Residues: 26-37 <JAC>
A;Cross-references: UNIPARC:UPI00001734E4
R;Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.
Eur. J. Biochem. 205, 311-319, 1992
A;Title: Isolation and characterization of two biologically active O-glycosylated forms
ation.
A;Reference number: S21199; MUID:92209518; PMID:1555591
A;Accession: S21199
A;Molecule type: protein
A;Residues: 32-114,'N' <OLS>
A;Cross-references: UNIPARC:UPI00001734E5
A;Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation,
R;Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L.H
Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974
A;Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid
A;Reference number: A93789; MUID:74111656; PMID:4521809
A;Accession: A93789
A;Molecule type: protein
A;Residues: 32-68 <NIA>
A;Cross-references: UNIPARC:UPI000002DA05
R;Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A;Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residues 1
A;Reference number: A93783; MUID:73070429; PMID:4509319
A;Accession: A93783
A;Molecule type: protein
A;Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <BRE>
A;Cross-references: UNIPARC:UPI00001734E6
A;Note: this sequence was determined by sequenator and mass spectroscopic identification
R;Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 14, 1842-1847, 1975
A;Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
A;Reference number: A90387; MUID:75146516; PMID:1125201
A;Accession: A90387
A;Molecule type: protein
A;Residues: 52-75 <KE3>
A;Cross-references: UNIPARC:UPI00001734E7
R;Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 17, 5723-5729, 1978
A;Title: Complete amino acid sequence of human parathyroid hormone.
A;Reference number: A90426; MUID:79082855; PMID:728431
A;Accession: A90426
A;Molecule type: protein
A;Residues: 61-106,'D',108-115 <KEU>
A;Cross-references: UNIPARC:UPI00001734E8
R;Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-
A;Reference number: A94410
A;Accession: A94410
A;Molecule type: protein
A;Residues: 75-100 <KE2>
A;Cross-references: UNIPARC:UPI00001734E9
R;Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J
Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
A;Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum
A;Reference number: A91660; MUID:75059220; PMID:4474131
A;Contents: annotation; synthesis of residues 32-65
A;Note: the biologically active amino-terminal 34 residues of parathyroid hormone were s
at renal adenylate cyclase assay and with the bovine hormone's active region in the chic
R;Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel,
Helv. Chim. Acta 56, 470-473, 1973
A;Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
A;Reference number: A91635; MUID:73227467; PMID:4721748
A;Contents: annotation; synthesis of residues 32-65
A;Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined
into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
R;Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
A;Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
A;Reference number: I38342; MUID:82150870; PMID:6950381
A;Accession: I38342
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: UNIPARC:UPI000013290A; EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PID
C;Genetics:
A;Gene: GDB:PTH
A;Cross-references: GDB:119522; OMIM:168450
A;Map position: 11p15.2-11p15.1
A;Introns: 29/2
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: factor in homeostatic control of plasma calcium and phosphate; released b
counter to calcitonin
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland; plasma
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 78.1%; Score 125; DB 1; Length 115;
Best Local Similarity 83.9%; Pred. No. 1.9e-09;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
:|||||||| | ||||||||||||||||
Db 32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62

RESULT 2
PTBO
parathyroid hormone precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534
R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.
Gene 28, 319-329, 1984
A;Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroid ho
A;Reference number: A24949; MUID:84262483; PMID:6086460
A;Accession: A24949
A;Molecule type: DNA
A;Residues: 1-115 <WEA>
A;Cross-references: UNIPROT:P01268; UNIPARC:UPI0000132907; GB:K01938
R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr.,
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979
A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid horm
A;Reference number: A93835; MUID:80056617; PMID:388425
A;Accession: A93835
A;Molecule type: DNA
A;Residues: 1-115 <KRO>
A;Cross-references: UNIPARC:UPI0000132907; GB:V00106; GB:J00023; NID:g84; PIDN:CAA23439.1
A;Note: the authors translated the codon GAA for residue 50 as Gly
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.V.
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974
A;Title: The N-terminal amino-acid sequence of bovine proparathyroid hormone.
A;Reference number: A93793; MUID:74142666; PMID:4522780
A;Accession: A93793
A;Molecule type: protein
A;Residues: 26-115 <HAM>
A;Cross-references: UNIPARC:UPI00001734DF
R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; Potts
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970
A;Title: The amino acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162; PMID:5531031
A;Accession: A91648
A;Molecule type: protein
A;Residues: 32-115 <NIA>
A;Cross-references: UNIPARC:UPI00000473E4
R;Brewer Jr., H.B.; Ronan, R.
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970
A;Title: Bovine parathyroid hormone: amino acid sequence.
A;Reference number: A93773; MUID:71063634; PMID:5275384
A;Accession: A93773
A;Molecule type: protein
A;Residues: 32-115 <BRE>
A;Cross-references: UNIPARC:UPI00000473E4
R;Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.;
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
A;Title: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyro
A;Reference number: A93776; MUID:71091588; PMID:4322265
A;Contents: annotation; synthesis of residues 32-65
A;Note: the synthetic peptide was active in vivo and in vitro
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
R;Weaver, C.A.; Gordon, D.F.
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
A;Title: introduction by molecular cloning of artifactual inverted sequences at the 5' te
A;Reference number: I45975; MUID:82037785; PMID:6170060
A;Accession: I45975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE2>
A;Cross-references: UNIPARC:UPI0000132907; GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:g
R;Weaver, C.A.; Gordon, D.F.

Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: I45976; MUID:83105964; PMID:6185374
A;Accession: I45976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE3>
A;Cross-references: UNIPARC:UPI0000132907; GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:
C;Genetics:
A;Gene: PTH
A;Introns: 29/2
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-115/Product: proparathyroid hormone #status experimental <PMAT>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 74.4%; Score 119; DB 1; Length 115;
Best Local Similarity 80.6%; Pred. No. 1.2e-08;
Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
||||||||| | |:|||||||||||||||
Db 32 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62

RESULT 3
PTPG
parathyroid hormone precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: B26806; A90390; A90376; A01535
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: B26806
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: UNIPROT:P01269; UNIPARC:UPI000013290B; GB:X05722; GB:Y00409; NID:g18
R;Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Biochemistry 14, 3631-3635, 1975
A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial amino
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Accession: A90390
A;Molecule type: protein
A;Residues: 26-115 <CHU>
A;Cross-references: UNIPARC:UPI00001592DF
R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J
Biochemistry 13, 1994-1999, 1974
A;Title: The amino acid sequence of porcine parathyroid hormone.
A;Reference number: A90376; MUID:74253317; PMID:4840833
A;Accession: A90376
A;Molecule type: protein
A;Residues: 32-109 <SAU>
A;Cross-references: UNIPARC:UPI00001734E0
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormon
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 73.1%; Score 117; DB 1; Length 115;
Best Local Similarity 77.4%; Pred. No. 2.1e-08;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
:|||||||| | |:|:||||||||||||
Db 32 SVSEIQLMHNLGKHLSSLERVEWLRKKLQDV 62

RESULT 4
JC4202
parathyroid hormone precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C;Accession: JC4202
R;Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.C.
Gene 160, 241-243, 1995
A;Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein and
A;Reference number: JC4201; MUID:95369696; PMID:7642102
A;Accession: JC4202
A;Molecule type: mRNA
A;Residues: 1-115 <ROS>
A;Cross-references: UNIPROT:P52212; UNIPARC:UPI0000132908; GB:U15662; NID:g558915; PIDN:
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-31/Domain: signal sequence #status predicted <SIG>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status predicted <MAT>

Query Match 72.5%; Score 116; DB 2; Length 115;
Best Local Similarity 77.4%; Pred. No. 2.9e-08;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
:||||| || | |:|||||||||||||||
Db 32 SVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62

RESULT 5
A05091
parathyroid hormone precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05091; A26806
R;Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
J. Biol. Chem. 259, 3320-3329, 1984
A;Reference number: A05091; MUID:84135846; PMID:6321505
A;Accession: A05091
A;Molecule type: DNA
A;Residues: 1-115 <HEI>
A;Cross-references: UNIPROT:P04089; UNIPARC:UPI000013290C; GB:K01268; NID:g206483; PIDN:
A;Note: the authors translated the codon GAA for residue 87 as Asp
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: A26806
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: UNIPARC:UPI000013290C; GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA291
C;Genetics:
A;Introns: 29/3
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;30-64/Domain: parathyroid hormone homology <PTH>

Query Match 68.8%; Score 110; DB 2; Length 115;
Best Local Similarity 74.2%; Pred. No. 1.8e-07;
Matches 23; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
||||||||| | | |:||::||||||||||
Db 32 AVSEIQLMHNLGKHLASVERMQWLRKKLQDV 62

```
RESULT 6
I51851
parathyroid hormone - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I51851
R;Schmelzer, H.
Adv. Gene Technol. 21, 228-229, 1984
A;Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A;Reference number: I51851
A;Accession: I51851
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-105 <RES>
A;Cross-references: UNIPARC:UPI0000170AE0; GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:
C;Genetics:
A;Gene: PTH
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;20-54/Domain: parathyroid hormone homology <PTH>

  Query Match             65.6%;  Score 105;  DB 2;  Length 105;
  Best Local Similarity   70.0%;  Pred. No. 7.5e-07;
  Matches   21;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQD 30
              |:|||||||  |  | |:||::||||||||
Db         22 AISEIQLMHNLGKHLASVERMQWLRKKLQD 51


RESULT 7
A34937
parathyroid hormone precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: A34937; I50411
R;Russell, J.; Sherwood, L.M.
Mol. Endocrinol. 3, 325-331, 1989
A;Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyro
A;Reference number: A34937; MUID:89219100; PMID:2710135
A;Accession: A34937
A;Molecule type: mRNA
A;Residues: 1-119 <RUS>
A;Cross-references: UNIPROT:P15743; UNIPARC:UPI0000132909; GB:M31604; NID:g212767; PIDN:
R;Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.
J. Bone Miner. Res. 3, 689-698, 1988
A;Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.
A;Reference number: I50411; MUID:89284968; PMID:3251402
A;Accession: I50411
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-119 <KHO>
A;Cross-references: UNIPARC:UPI0000132909; GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status predicted <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-119/Product: parathyroid hormone #status predicted <MAT>

  Query Match             53.1%;  Score 85;  DB 2;  Length 119;
  Best Local Similarity   54.8%;  Pred. No. 0.00037;
  Matches   17;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||:|||| |   :::|| :||: |||||
Db         32 SVSEMQLMHNLGEHRHTVERQDWLQMKLQDV 62


RESULT 8
B43777
choline O-acetyltransferase (EC 2.3.1.6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accession: B43777; A44023
R;Ishii, K.; Oda, Y.; Ichikawa, T.; Deguchi, T.
Brain Res. Mol. Brain Res. 7, 151-159, 1990
A;Title: Complementary DNAs for choline acetyltransferase from spinal cords of rat and mo
A;Reference number: A43777; MUID:90251122; PMID:2160042
A;Accession: B43777
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-641 <ISH>
A;Cross-references: UNIPROT:Q03059; UNIPARC:UPI000017535E
R;Misawa, H.; Ishii, K.; Deguchi, T.
J. Biol. Chem. 267, 20392-20399, 1992
A;Title: Gene expression of mouse choline acetyltransferase. Alternative splicing and ide
A;Reference number: A44023; MUID:93015919; PMID:1400357
A;Accession: A44023
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA; mRNA
A;Residues: 1-219 <MIS>
A;Cross-references: UNIPARC:UPI000016CC80; GB:D12487; NID:g220366; PIDN:BAA02056.1; PID:g
A;Note: sequence extracted from NCBI backbone (NCBIP:115801)
C;Superfamily: carnitine O-acetyltransferase
C;Keywords: acyltransferase; coenzyme A

  Query Match             38.8%;  Score 62;  DB 2;  Length 641;
  Best Local Similarity   51.9%;  Pred. No. 2.3;
  Matches   14;  Conservative    2;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          5 IQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||:|||| ||   |  |  | || |
Db        298 LQLLHGGGCSLNGANR--WYDKSLQFV 322


RESULT 9
A48319
choline O-acetyltransferase (EC 2.3.1.6) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48319; A43777; A48981; A56876
R;Brice, A.; Berrard, S.; Raynaud, B.; Ansieau, S.; Coppola, T.; Weber, M.J.; Mallet, J.
J. Neurosci. Res. 23, 266-273, 1989
A;Title: Complete sequence of a cDNA encoding an active rat choline acetyltransferase: a
A;Reference number: A48319; MUID:89362560; PMID:2570161
A;Accession: A48319
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-644 <BRI>
A;Cross-references: UNIPROT:P32738; UNIPARC:UPI000017535A
R;Ishii, K.; Oda, Y.; Ichikawa, T.; Deguchi, T.
Brain Res. Mol. Brain Res. 7, 151-159, 1990
A;Title: Complementary DNAs for choline acetyltransferase from spinal cords of rat and mo
A;Reference number: A43777; MUID:90251122; PMID:2160042
A;Accession: A43777
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-233,'N',235-376,'L',378-498,'HKQ',502-569,'N',571-634,'SQAKQS' <ISH>
A;Cross-references: UNIPARC:UPI000017535B
R;Mori, N.; Tajima, Y.; Sakaguchi, H.; Vandenbergh, D.J.; Nawa, H.; Salvaterra, P.M.
Brain Res. Mol. Brain Res. 17, 101-111, 1993
A;Title: Partial cloning of the rat choline acetyltransferase gene and in situ localizati
A;Reference number: A48981; MUID:93164851; PMID:8381893
A;Accession: A48981
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 397-437 <MOR>
A;Cross-references: UNIPARC:UPI000017535C
A;Note: sequence extracted from NCBI backbone (NCBIN:124964, NCBIP:124965)
R;Kengaku, M.; Misawa, H.; Deguchi, T.
Brain Res. Mol. Brain Res. 18, 71-76, 1993
A;Title: Multiple mRNA species of choline acetyltransferase from rat spinal cord.
A;Reference number: A56876; MUID:93240983; PMID:8479291
A;Accession: A56876
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-33 <KEN>
```

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A;Cross-references: UNIPARC:UPI000017535D
A;Experimental source: spinal cord
A;Note: sequence extracted from NCBI backbone (NCBIN:130081, NCBIP:130082)
C;Superfamily: carnitine O-acetyltransferase
C;Keywords: acyltransferase; coenzyme A

  Query Match             38.8%;  Score 62;  DB 2;  Length 644;
  Best Local Similarity   51.9%;  Pred. No. 2.3;
  Matches   14;  Conservative    2;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          5 IQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||:||||  ||   |  |  | || |
Db        297 LQLLHGGGCSLNGANR--WYDKSLQFV 321


RESULT 10
A55720
carnitine O-acetyltransferase (EC 2.3.1.7) precursor, mitochondrial - human
N;Alternate names: cat1 protein
N;Contains: carnitine O-acetyltransferase, peroxisomal
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A55720; S50030; S50029
R;Corti, O.; Finocchiaro, G.; Rossi, E.; Zuffardi, O.; DiDonato, S.
Genomics 23, 94-99, 1994
A;Title: Molecular cloning of cDNAs encoding human carnitine acetyltransferase and mappi
A;Reference number: A55720; MUID:95130117; PMID:7829107
A;Accession: A55720
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 22-626 <CO2>
A;Cross-references: UNIPROT:P43155; UNIPARC:UPI000002A53F; EMBL:X78706
R;Corti, O.; DiDonato, S.; Finocchiaro, G.
Biochem. J. 303, 37-41, 1994
A;Title: Divergent sequences in the 5' region of cDNA suggest alternative splicing as a
A;Reference number: S50029; MUID:95031982; PMID:7945262
A;Accession: S50030
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-52 <COR>
A;Cross-references: UNIPARC:UPI000017535F; EMBL:X79825
A;Experimental source: clone SM-1200
A;Accession: S50029
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 22-52 <CO3>
A;Cross-references: UNIPARC:UPI0000175360; EMBL:X79827
A;Experimental source: clone SM-1400
C;Genetics:
A;Gene: GDB:CRAT; CAT1
A;Cross-references: GDB:359759; OMIM:600184
A;Map position: 9q34.1-9q34.1
A;Note: at least one intron occurs before the initiator of the peroxisomal form
C;Superfamily: carnitine O-acetyltransferase
C;Keywords: acyltransferase; alternative splicing; coenzyme A; mitochondrion; peroxisome
F;1-626/Product: carnitine O-acetyltransferase precursor, mitochondrial splice form #sta
F;1-28/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;22-626/Product: carnitine O-acetyltransferase precursor, peroxisomal splice form #stat
F;22-29/Domain: propeptide #link MATP #status predicted <PRO>
F;29-626/Product: carnitine O-acetyltransferase, mitochondrial #status predicted <MATM>
F;30-626/Product: carnitine O-acetyltransferase, peroxisomal #status predicted <MATP>
F;624-626/Region: peroxisome/glyoxysome location signal #status atypical

  Query Match             37.5%;  Score 60;  DB 2;  Length 626;
  Best Local Similarity   54.2%;  Pred. No. 4.1;
  Matches   13;  Conservative    2;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          6 QLMHGGGGGLNSMERVEWLRKKLQ 29
              |::||||  |||  |  |  | ||
Db        307 QMLHGGGSRLNSGNR--WFDKTLQ 328


RESULT 11
T03784
probable receptor protein kinase - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C;Accession: T03784
R;Xu, Y.; Zhu, Q.; Lamb, C.
submitted to the EMBL Data Library, June 1995
A;Description: Molecular cloning and characterization of a rice gene encoding leucine-ri
A;Reference number: Z15083
A;Accession: T03784
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-990 <XUY>
A;Cross-references: UNIPROT:Q40699; UNIPARC:UPI00000A9030; EMBL:X89226; NID:g1263159; PI
A;Experimental source: cv. IR36, leaf
C;Genetics:
A;Gene: lrk2
A;Introns: 870/1
C;Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat ho

  Query Match             36.9%;  Score 59;  DB 2;  Length 990;
  Best Local Similarity   52.4%;  Pred. No. 8.9;
  Matches   11;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          8 MHGGGGGLNSMERVEWLRKKL 28
              | |||||  |  |: |  ||:
Db        625 MRGGGGGAGSQLRLRWDSKKM 645


RESULT 12
D69651
PTS lichenan-specific enzyme IIA component licA - Bacillus subtilis
N;Alternate names: probable cellobiose phosphotransferase enzyme III
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 31-Dec-2004
C;Accession: D69651; S57761
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D69651
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-110 <KUN>
A;Cross-references: UNIPROT:P46319; UNIPARC:UPI0000060C4F; GB:Z99123; GB:AL009126; NID:g
A;Experimental source: strain 168
R;Glaser, P.; Lubochinsky, B.; Danchin, A.
submitted to the EMBL Data Library, July 1995
A;Description: Bacillus subtilis cel operon.
A;Reference number: S57758
A;Accession: S57761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <GLA>
A;Cross-references: UNIPARC:UPI0000060C4F; EMBL:Z49992; NID:g895746; PIDN:CAA90287.1; PI
C;Genetics:
A;Gene: licA
A;Start codon: GTG
C;Superfamily: phosphotransferase system, lactose/cellobiose-specific component IIA

  Query Match             35.6%;  Score 57;  DB 2;  Length 110;
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```
  Best Local Similarity   40.6%;  Pred. No. 1.7;
  Matches   13;  Conservative    5;  Mismatches    6;  Indels    8;  Gaps    1;

Qy          7 LMHGGGGGLNSMERV--------EWLRKKLQD 30
              ::||| |  ::|| :        |  ||||||
Db         13 ILHGGNGRSSAMEAIAAAKSGDAEEARKKLQD 44


RESULT 13
HMXRH2
sigma 1 protein - reovirus type 2
N;Alternate names: hemagglutinin
C;Species: reovirus type 2
A;Note: host Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A04123
R;Cashdollar, L.W.; Chmelo, R.A.; Wiener, J.R.; Joklik, W.K.
Proc. Natl. Acad. Sci. U.S.A. 82, 24-28, 1985
A;Title: Sequences of the S1 genes of the three serotypes of reovirus.
A;Reference number: A94035; MUID:85113159; PMID:3855545
A;Accession: A04123
A;Molecule type: genomic RNA
A;Residues: 1-399 <CAS>
A;Cross-references: UNIPROT:P04507; UNIPARC:UPI0000163913; GB:M10261; NID:g808813; PIDN:
C;Genetics:
A;Gene: S1; sigma 1
C;Superfamily: reovirus sigma 1 protein
C;Keywords: glycoprotein; hemagglutinin
F;237,243,297/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             35.0%;  Score 56;  DB 1;  Length 399;
  Best Local Similarity   35.7%;  Pred. No. 8.8;
  Matches   10;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 EIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              || |: | |   ||   :| ::|:::|:
Db         11 EILLLTGNGESANSKHEIEEIKKQIKDI 38


RESULT 14
C34829
sigma 1 protein - reovirus type 2 (strain Jones)
N;Alternate names: hemagglutinin; minor outer capsid protein
C;Species: reovirus type 2
A;Note: host Homo sapiens (man)
C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 09-Jul-2004
C;Accession: C34829
R;Nibert, M.L.; Dermody, T.S.; Fields, B.N.
J. Virol. 64, 2976-2989, 1990
A;Title: Structure of the reovirus cell-attachment protein: a model for the domain organ
A;Reference number: A34829; MUID:90244415; PMID:2335823
A;Accession: C34829
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-462 <NIB>
A;Cross-references: UNIPROT:Q85663; UNIPARC:UPI00000EFB2C; GB:M35964; NID:g333671; PIDN:
C;Genetics:
A;Map position: segment S1
C;Superfamily: reovirus sigma 1 protein

  Query Match             35.0%;  Score 56;  DB 2;  Length 462;
  Best Local Similarity   35.7%;  Pred. No. 10;
  Matches   10;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 EIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              || |: | |   ||   :| ::|:::|:
Db         11 EILLLTGNGESANSKHEIEEIKKQIKDI 38


RESULT 15
S52782
carnitine acetyltransferase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52782
R;Brunner, S.; Kramar, K.; Hofbauer, R.
submitted to the EMBL Data Library, March 1995
A;Description: A novel cell cycle regulated carnitine acetyltransferase in S3T3 cells.
A;Reference number: S52782
A;Accession: S52782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-627 <BRU>
A;Cross-references: UNIPROT:P47934; UNIPARC:UPI000002783E; EMBL:X85983; NID:g758631; PIDN
C;Superfamily: carnitine O-acetyltransferase

  Query Match             35.0%;  Score 56;  DB 2;  Length 627;
  Best Local Similarity   50.0%;  Pred. No. 14;
  Matches   12;  Conservative    2;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          6 QLMHGGGGGLNSMERVEWLRKKLQ 29
              |::||||   ||  |  |  | ||
Db        308 QMLHGGGSKFNSGNR--WFDKTLQ 329


Search completed: November 21, 2005, 16:17:15
Job time : 24.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 15:55:27 ; Search time 146.5 Seconds
(without alignments)
149.293 Million cell updates/sec

Title: US-09-475-158A-3
Perfect score: 160
Sequence: 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	125	78.1	115	1	PTHY_HUMAN	P01270 homo sapien
2	125	78.1	115	1	PTHY_MACFA	Q9xt35 macaca fasc
3	125	78.1	115	2	Q4VB48_HUMAN	Q4vb48 homo sapien
4	121	75.6	86	2	Q9N1V0_HORSE	Q9n1v0 equus cabal
5	119	74.4	115	1	PTHY_BOVIN	P01268 bos taurus
6	117	73.1	115	1	PTHY_PIG	P01269 sus scrofa
7	116	72.5	115	1	PTHY_CANFA	P52212 canis famil
8	110	68.8	105	2	Q80WZ2_RAT	Q80wz2 rattus norv
9	110	68.8	115	1	PTHY_RAT	P04089 rattus norv
10	109	68.1	115	1	PTHY_FELCA	Q9gl67 felis silve
11	108	67.5	115	2	Q9Z0L6_MOUSE	Q9z0l6 mus musculu
12	85	53.1	119	1	PTHY_CHICK	P15743 gallus gall
13	68	42.5	91	2	Q6W9J4_FUGRU	Q6w9j4 fugu rubrip
14	65	40.6	15	1	CB30_HYDMC	P83630 hydrangea m
15	65	40.6	163	2	Q9I8E9_FUGRU	Q9i8e9 fugu rubrip
16	63	39.4	166	2	Q6H9R6_PLAFE	Q6h9r6 platichthys
17	63	39.4	166	2	Q53IQ0_PLAFE	Q53iq0 platichthys
18	62	38.8	99	2	Q6WQ24_BRARE	Q6wq24 brachydanio
19	62	38.8	162	2	Q9I8U2_SPAAU	Q9i8u2 sparus aura
20	62	38.8	250	1	BIOH_AZOSE	Q5nzf6 azoarcus sp
21	62	38.8	625	2	Q8BQN4_MOUSE	Q8bqn4 mus musculu
22	62	38.8	639	1	CLAT_RAT	P32738 rattus norv
23	62	38.8	640	1	CLAT_MOUSE	Q03059 mus musculu
24	62	38.8	645	2	Q8BQV2_MOUSE	Q8bqv2 mus musculu
25	60	37.5	102	2	Q5TLZ1_BRARE	Q5tlz1 brachydanio
26	60	37.5	102	2	Q6WQ25_BRARE	Q6wq25 brachydanio
27	60	37.5	107	2	Q4TGY4_TETNG	Q4tgy4 tetraodon n
28	60	37.5	530	2	Q4SRM4_TETNG	Q4srm4 tetraodon n
29	60	37.5	626	1	CACP_HUMAN	P43155 homo sapien
30	60	37.5	626	2	Q5T952_HUMAN	Q5t952 homo sapien
31	59	36.9	990	2	Q40699_ORYSA	Q40699 oryza sativ
32	58	36.2	177	2	Q4RSF3_TETNG	Q4rsf3 tetraodon n
33	57	35.6	31	2	Q91Y90_PERMA	Q91y90 peromyscus
34	57	35.6	31	2	Q91Y91_PERPL	Q91y91 peromyscus
35	57	35.6	110	1	PTJA_BACSU	P46319 bacillus su
36	57	35.6	208	2	Q6FT33_CANGA	Q6ft33 candida gla
37	57	35.6	549	2	Q4J3M6_AZOVI	Q4j3m6 azotobacter
38	57	35.6	631	2	Q642H6_BRARE	Q642h6 brachydanio
39	57	35.6	994	2	Q5Z9N5_ORYSA	Q5z9n5 oryza sativ
40	57	35.6	994	2	Q8SB35_ORYSA	Q8sb35 oryza sativ
41	57	35.6	1449	2	Q4RPY8_TETNG	Q4rpy8 tetraodon n
42	56.5	35.3	232	2	Q6H658_ORYSA	Q6h658 oryza sativ
43	56	35.0	198	2	Q5SPK3_BRARE	Q5spk3 brachydanio
44	56	35.0	198	2	Q4VVA3_BRARE	Q4vva3 brachydanio
45	56	35.0	293	2	Q9FJJ5_ARATH	Q9fjj5 arabidopsis

ALIGNMENTS

RESULT 1
PTHY_HUMAN
ID PTHY_HUMAN STANDARD; PRT; 115 AA.
AC P01270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).
GN Name=PTH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82150870; PubMed=6950381;
RA Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;
RT "Nucleotide sequence of cloned cDNAs encoding human preproparathyroid
RT hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83169834; PubMed=6220408;
RA Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J., Hendy G.N.,
RA Potts J.T. Jr., Rich A., Kronenberg H.M.;
RT "Nucleotide sequence of the human parathyroid hormone gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
RN [3]
RP PROTEIN SEQUENCE OF 26-37.
RX MEDLINE=74174967; PubMed=4833516;
RA Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;
RT "Structural analysis of human proparathyroid hormone by a new
RT microsequencing approach.";
RL Nature 249:155-157(1974).
RN [4]
RP PROTEIN SEQUENCE OF 26-40.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [5]
RP PROTEIN SEQUENCE OF 32-68.
RX MEDLINE=74111656; PubMed=4521809;
RA Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
RA O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;
RT "The amino-acid sequence of the amino-terminal 37 residues of human
RT parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).
RN [6]
RP PROTEIN SEQUENCE OF 61-83 AND 84-115.
RX MEDLINE=79082855; PubMed=728431;
RA Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,

```
RA   Potts J.T. Jr.;
RT   "Complete amino acid sequence of human parathyroid hormone.";
RL   Biochemistry 17:5723-5729(1978).
RN   [7]
RP   PROTEIN SEQUENCE OF 75-100.
RA   Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,
RA   O'Riordan J.L.H., Potts J.T. Jr.;
RL   (In) Talmadge R.V., Owen M., Parsons J.A. (eds.);
RL   Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,
RL   Amsterdam (1975).
RN   [8]
RP   SEQUENCE REVISION.
RX   MEDLINE=75146516; PubMed=1125201;
RA   Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "A reinvestigation of the amino-terminal sequence of human parathyroid
RT   hormone.";
RL   Biochemistry 14:1842-1847(1975).
RN   [9]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=75059220; PubMed=4474131;
RA   Tregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T.,
RA   Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "Solid-phase synthesis of the biologically active N-terminal 1-34
RT   peptide of human parathyroid hormone.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
RN   [10]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=73227467; PubMed=4721748;
RA   Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
RA   Riniker B., Rittel W., Sieber P.;
RT   "Synthesis of sequence 1-34 of human parathyroid hormone.";
RL   Helv. Chim. Acta 56:470-473(1973).
RN   [11]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=91299748; PubMed=2069952;
RA   Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
RT   "Investigation of the solution structure of the human parathyroid
RT   hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and
RT   molecular dynamics calculations.";
RL   Biochemistry 30:6936-6942(1991).
RN   [12]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=93345518; PubMed=8344299;
RA   Barden J.A., Cuthbertson R.M.;
RT   "Stabilized NMR structure of human parathyroid hormone(1-34).";
RL   Eur. J. Biochem. 215:315-321(1993).
RN   [13]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;
RA   Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
RA   Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
RA   Roesch P.;
RT   "Structure of human parathyroid hormone 1-37 in solution.";
RL   J. Biol. Chem. 270:15194-15202(1995).
RN   [14]
RP   STRUCTURE BY NMR OF 32-70.
RX   MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments hPTH(1-34)
RT   and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
RN   [15]
RP   VARIANT FIH ARG-18.
RX   MEDLINE=91009811; PubMed=2212001;
RA   Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
RA   Kronenberg H.M.;
RT   "Mutation of the signal peptide-encoding region of the
RT   preproparathyroid hormone gene in familial isolated
RT   hypoparathyroidism.";
RL   J. Clin. Invest. 86:1084-1087(1990).
RN   [16]
RP   VARIANT FIH PRO-23.
RX   PubMed=10523031;
RA   Sunthornthepvarakul T., Churesigaew S., Ngowngarmratana S.;
RT   "A novel mutation of the signal peptide of the preproparathyroid
RT   hormone gene associated with autosomal recessive familial isolated
RT   hypoparathyroidism.";
RL   J. Clin. Endocrinol. Metab. 84:3792-3796(1999).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- DISEASE: Defects in PTH are a cause of familial isolated
CC       hypoparathyroidism (FIH) [MIM:146200]. FIH exist both as autosomal
CC       dominant and recessive forms of hypoparathyroidism.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; J00301; AAA60215.1; -; Genomic_DNA.
DR   EMBL; V00597; CAA23843.1; -; mRNA.
DR   EMBL; A29146; CAA01956.1; -; Unassigned_DNA.
DR   PIR; A19339; PTHU.
DR   PDB; 1BWX; NMR; @=32-70.
DR   PDB; 1ET1; X-ray; A/B=32-65.
DR   PDB; 1ET2; Model; A=32-65.
DR   PDB; 1FVY; NMR; A=32-62.
DR   PDB; 1HPH; NMR; @=32-68.
DR   PDB; 1HPY; NMR; @=32-65.
DR   PDB; 1HTH; NMR; @=32-65.
DR   PDB; 1ZWA; NMR; @=32-65.
DR   PDB; 1ZWB; NMR; @=33-68.
DR   PDB; 1ZWD; NMR; @=34-68.
DR   PDB; 1ZWE; NMR; @=35-68.
DR   PDB; 1ZWF; NMR; @=35-68.
DR   PDB; 1ZWG; NMR; @=-.
DR   Ensembl; ENSG00000152266; Homo sapiens.
DR   HGNC; HGNC:9606; PTH.
DR   MIM; 168450; -.
DR   MIM; 146200; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   GO; GO:0045453; P:bone resorption; NAS.
DR   GO; GO:0006874; P:calcium ion homeostasis; NAS.
DR   GO; GO:0046058; P:cAMP metabolism; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
DR   GO; GO:0001501; P:skeletal development; TAS.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   3D-structure; Direct protein sequencing; Disease mutation; Hormone;
KW   Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
FT   VARIANT      18     18       C -> R (in FIH; dominant; leads to
FT                                inefficient processing of the precursor).
FT                                /FTId=VAR_006047.
FT   VARIANT      23     23       S -> P (in FIH; recessive, might lead to
FT                                inefficient processing of the precursor).
FT                                /FTId=VAR_018464.
FT   CONFLICT    107    107       N -> D (in Ref. 6).
FT   HELIX        34     64
SQ   SEQUENCE   115 AA;  12861 MW;  849015736A6E5597 CRC64;
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Query Match 78.1%; Score 125; DB 1; Length 115;

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  Best Local Similarity   83.9%;  Pred. No. 1.3e-08;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| | ||||||||||||||||
Db         32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62


RESULT 2
PTHY_MACFA
ID   PTHY_MACFA     STANDARD;      PRT;   115 AA.
AC   Q9XT35;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Malaivijitnond S., Takenaka O.;
RT   "Nucleotide sequences of parathyroid gene in five species of macaque
RT   of Thailand.";
RL   J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AF130257; AAD42777.1; -; Genomic_DNA.
DR   HSSP; P01270; 1ET1.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       By similarity.
FT   PROPEP       26     31       By similarity.
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12890 MW;  8C2500EF24BE5597 CRC64;

  Query Match             78.1%;  Score 125;  DB 1;  Length 115;
  Best Local Similarity   83.9%;  Pred. No. 1.3e-08;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| | ||||||||||||||||
Db         32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62


RESULT 3
Q4VB48_HUMAN
ID   Q4VB48_HUMAN PRELIMINARY;      PRT;   115 AA.
AC   Q4VB48;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Parathyroid hormone, preproprotein.
GN   Name=PTH;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC096143; AAH96143.1; -; mRNA.
DR   EMBL; BC096144; AAH96144.1; -; mRNA.
DR   EMBL; BC096145; AAH96145.1; -; mRNA.
DR   EMBL; BC096142; AAH96142.1; -; mRNA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
SQ   SEQUENCE   115 AA;  12861 MW;  849015736A6E5597 CRC64;

  Query Match             78.1%;  Score 125;  DB 2;  Length 115;
  Best Local Similarity   83.9%;  Pred. No. 1.3e-08;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| | ||||||||||||||||
Db         32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62


RESULT 4
Q9N1V0_HORSE
ID   Q9N1V0_HORSE PRELIMINARY;      PRT;    86 AA.
AC   Q9N1V0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Parathyroid hormone (Fragment).
GN   Name=PTH;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;
RA   Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
```

```
RA   Bowling A.T., Murray J.D.;
RT   "A comparative gene map of the horse (Equus caballus).";
RL   Genome Res. 9:1239-1249(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Shiue Y.-L., Caetano A.R., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Murray J.D., Bowling A.T.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF134233; AAF62347.1; -; Genomic_DNA.
DR   HSSP; P01270; 1ET1.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   86 AA;  9805 MW;  253184EA681A2022 CRC64;

  Query Match             75.6%;  Score 121;  DB 2;  Length 86;
  Best Local Similarity   80.6%;  Pred. No. 3.2e-08;
  Matches   25;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||  |  |||:|||||||||||||
Db          3 SVSEIQLMHNLGKHLNSVERVEWLRKKLQDV 33


RESULT 5
PTHY_BOVIN
ID   PTHY_BOVIN     STANDARD;      PRT;   115 AA.
AC   P01268;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=80056617; PubMed=388425;
RA   Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA   Potts J.T. Jr., Rich A.;
RT   "Cloning and nucleotide sequence of DNA coding for bovine
RT   preproparathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82037785; PubMed=6170060;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Introduction by molecular cloning of artifactual inverted sequences
RT   at the 5' terminus of the sense strand of bovine parathyroid hormone
RT   cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL   Mol. Cell. Endocrinol. 28:411-424(1982).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84262483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
RA   Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT   "Isolation and complete nucleotide sequence of the gene for bovine
RT   parathyroid hormone.";
RL   Gene 28:319-329(1984).
RN   [5]
RP   PROTEIN SEQUENCE OF 26-115.
RX   MEDLINE=74142666; PubMed=4522780;
RA   Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA   Cohn D.V.;
RT   "The N-terminal amino-acid sequence of bovine proparathyroid
RT   hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN   [6]
RP   PROTEIN SEQUENCE OF 32-115.
RX   MEDLINE=71076162; PubMed=5531031;
RA   Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
RA   Aurbach G.D., Potts J.T. Jr.;
RT   "The amino acid sequence of bovine parathyroid hormone I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN   [7]
RP   PROTEIN SEQUENCE OF 32-115.
RX   MEDLINE=71063634; PubMed=5275384;
RA   Brewer H.B. Jr., Ronan R.;
RT   "Bovine parathyroid hormone: amino acid sequence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN   [8]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=71091588; PubMed=4322265;
RA   Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA   Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT   "Synthesis of a biologically active N-terminal tetratriacontapeptide
RT   of parathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN   [9]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments hPTH(1-34)
RT   and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   EMBL; V00106; CAA23439.1; -; mRNA.
DR   EMBL; J00024; AAA30747.1; -; mRNA.
DR   EMBL; K01938; AAA30749.1; -; Genomic_DNA.
DR   EMBL; M25082; AAA30748.1; -; mRNA.
DR   PIR; A24949; PTBO.
DR   PDB; 1ZWC; NMR; @=32-68.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   3D-structure; Direct protein sequencing; Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
FT   CONFLICT    106    106       V -> G (in Ref. 4).
FT   HELIX        37     40
FT   TURN         41     42
FT   TURN         51     52
FT   HELIX        53     60
FT   TURN         61     63
SQ   SEQUENCE   115 AA;  12980 MW;  2ED246B348880710 CRC64;
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  Query Match             74.4%;  Score 119;  DB 1;  Length 115;
  Best Local Similarity   80.6%;  Pred. No. 8e-08;
  Matches   25;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||| ||  |  |:|||||||||||||||
Db         32 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62


RESULT 6
PTHY_PIG
ID   PTHY_PIG       STANDARD;      PRT;   115 AA.
AC   P01269;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [2]
RP   PROTEIN SEQUENCE OF 26-115.
RX   MEDLINE=76018954; PubMed=1164500;
RA   Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
RT   "Porcine proparathyroid hormone. Identification, biosynthesis, and
RT   partial amino acid sequence.";
RL   Biochemistry 14:3631-3635(1975).
RN   [3]
RP   PROTEIN SEQUENCE OF 32-115.
RX   MEDLINE=74253317; PubMed=4840833;
RA   Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA   Potts J.T. Jr.;
RT   "The amino acid sequence of porcine parathyroid hormone.";
RL   Biochemistry 13:1994-1999(1974).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X05722; CAA29193.1; -; mRNA.
DR   PIR; B26806; PTPG.
DR   HSSP; P01270; 1BWX.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Direct protein sequencing; Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12852 MW;  9FE8BCDE614BAC16 CRC64;

  Query Match             73.1%;  Score 117;  DB 1;  Length 115;
  Best Local Similarity   77.4%;  Pred. No. 1.5e-07;
  Matches   24;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||  |  |:|:||||||||||||||
Db         32 SVSEIQLMHNLGKHLSSLERVEWLRKKLQDV 62


RESULT 7
PTHY_CANFA
ID   PTHY_CANFA     STANDARD;      PRT;   115 AA.
AC   P52212;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Parathyroid;
RX   MEDLINE=95369696; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;
RA   Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W.,
RA   Capen C.C.;
RT   "Sequences of the cDNAs encoding canine parathyroid hormone-related
RT   protein and parathyroid hormone.";
RL   Gene 160:241-243(1995).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U15662; AAA82584.1; -; mRNA.
DR   PIR; JC4202; JC4202.
DR   HSSP; P01268; 1ZWC.
DR   Ensembl; ENSCAFG00000008177; Canis familiaris.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       By similarity.
FT   PROPEP       26     31       By similarity.
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12957 MW;  FC38F77F1C8CFE56 CRC64;

  Query Match             72.5%;  Score 116;  DB 1;  Length 115;
  Best Local Similarity   77.4%;  Pred. No. 2e-07;
  Matches   24;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||  ||  |  |:|||||||||||||||
Db         32 SVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62


RESULT 8
Q80WZ2_RAT
ID   Q80WZ2_RAT  PRELIMINARY;      PRT;   105 AA.
```

```
AC   Q80WZ2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothalamic parathyroid hormone.
GN   Name=PTH-(1-84);
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA   Nutley M.T., Parimi S.A., Harvey S.;
RT   "Sequence analysis of hypothalamic parathyroid hormone messenger
RT   ribonucleic acid.";
RL   Endocrinology 136:5600-5607(1995).
DR   EMBL; S80127; AAP32220.1; -; mRNA.
DR   HSSP; P01270; 1ZWB.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
SQ   SEQUENCE   105 AA;  11684 MW;  18EE71B3F1CF5F70 CRC64;

  Query Match             68.8%;  Score 110;  DB 2;  Length 105;
  Best Local Similarity   74.2%;  Pred. No. 1.1e-06;
  Matches   23;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |   | |:||::|||||||||
Db         22 AVSEIQLMHNLGKHLASVERMQWLRKKLQDV 52


RESULT 9
PTHY_RAT
ID   PTHY_RAT       STANDARD;      PRT;   115 AA.
AC   P04089; Q63473;
DT   01-NOV-1986 (Rel. 03, Created)
DT   01-NOV-1986 (Rel. 03, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=Pth;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84135846; PubMed=6321505;
RA   Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT   "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
RT   gene and deduced amino acid sequence of rat preproparathyroid
RT   hormone.";
RL   J. Biol. Chem. 259:3320-3329(1984).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 10-115.
RC   TISSUE=Parathyroid;
RA   Schmelzer H.J., Gross G., Mayer H.;
RT   "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
RT   hormone.";
RL   Adv. Gene Technol. 21:228-229(1984).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 32-115.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
RX   MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA   Nutley M.T., Parimi S.A., Harvey S.;
RT   "Sequence analysis of hypothalamic parathyroid hormone messenger
RT   ribonucleic acid.";
RL   Endocrinology 136:5600-5607(1995).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Hypothalamus and parathyroid gland.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; K01268; AAA41979.1; -; Genomic_DNA.
DR   EMBL; X05721; CAA29192.1; -; mRNA.
DR   EMBL; M54875; AAA57156.1; -; mRNA.
DR   EMBL; S80127; -; NOT_ANNOTATED_CDS; mRNA.
DR   PIR; A05091; A05091.
DR   HSSP; P01270; 1ZWB.
DR   Ensembl; ENSRNOG00000014318; Rattus norvegicus.
DR   RGD; 3440; Pth.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003626; PTH_related.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD013225; PTH_related; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
FT   CONFLICT     18     18       C -> Y (in Ref. 3).
FT   CONFLICT     23     23       A -> T (in Ref. 3).
FT   CONFLICT     33     33       V -> I (in Ref. 3).
FT   CONFLICT     62     62       V -> G (in Ref. 3).
SQ   SEQUENCE   115 AA;  12722 MW;  7B434CFCA528B230 CRC64;

  Query Match             68.8%;  Score 110;  DB 1;  Length 115;
  Best Local Similarity   74.2%;  Pred. No. 1.3e-06;
  Matches   23;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |   | |:||::|||||||||
Db         32 AVSEIQLMHNLGKHLASVERMQWLRKKLQDV 62


RESULT 10
PTHY_FELCA
ID   PTHY_FELCA     STANDARD;      PRT;   115 AA.
AC   Q9GL67;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT   "Molecular cloning of feline preproparathyroid hormone.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF309967; AAG30545.1; -; mRNA.
DR   HSSP; P01268; 1ZWC.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       By similarity.
FT   PROPEP       26     31       By similarity.
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12921 MW;  80CD557CC6A1A47E CRC64;

  Query Match             68.1%;  Score 109;  DB 1;  Length 115;
  Best Local Similarity   71.0%;  Pred. No. 1.7e-06;
  Matches   22;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||||| ||  |  |:|:|||||||:|||||
Db         32 SVSEIQFMHNLGKHLSSVERVEWLRRKLQDV 62


RESULT 11
Q9Z0L6_MOUSE
ID   Q9Z0L6_MOUSE PRELIMINARY;      PRT;   115 AA.
AC   Q9Z0L6;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Parathyroid hormone precursor.
GN   Name=Pth;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/Sv;
RA   Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.;
RT   "Cloning of the murine gene encoding parathyroid hormone: genomic
RT   organization and nucleotide sequence.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thyroid;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF066075; AAC99656.1; -; Genomic_DNA.
DR   EMBL; BC099456; AAH99456.1; -; mRNA.
DR   HSSP; P01270; 1ZWB.
DR   Ensembl; ENSMUSG00000059077; Mus musculus.
DR   MGI; MGI:97799; Pth.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005179; F:hormone activity; IDA.
DR   GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Signal.
FT   SIGNAL        1     25       Potential.
FT   CHAIN        32    115       parathyroid hormone.
SQ   SEQUENCE   115 AA;  12825 MW;  DA43FABBCB4E2FD9 CRC64;

  Query Match             67.5%;  Score 108;  DB 2;  Length 115;
  Best Local Similarity   71.0%;  Pred. No. 2.3e-06;
  Matches   22;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |  | ||||::|||:||||:
Db         32 AVSEIQLMHNLGKHLASMERMQWLRRKLQDM 62


RESULT 12
PTHY_CHICK
ID   PTHY_CHICK     STANDARD;      PRT;   119 AA.
AC   P15743;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Parathyroid hormone precursor (PTH).
GN   Name=PTH;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89219100; PubMed=2710135;
RA   Russell J., Sherwood L.M.;
RT   "Nucleotide sequence of the DNA complementary to avian (chicken)
RT   preproparathyroid hormone mRNA and the deduced sequence of the hormone
RT   precursor.";
RL   Mol. Endocrinol. 3:325-331(1989).
```

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RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89284968; PubMed=3251402;
RA   Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
RA   Kronenberg H.M.;
RT   "Nucleotide sequence of cloned cDNAs encoding chicken
RT   preproparathyroid hormone.";
RL   J. Bone Miner. Res. 3:689-698(1988).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M31604; AAA49093.1; -; mRNA.
DR   EMBL; M36522; AAB02866.1; -; mRNA.
DR   PIR; A34937; A34937.
DR   HSSP; P01270; 1FVY.
DR   Ensembl; ENSGALG00000005358; Gallus gallus.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003626; PTH_related.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD013225; PTH_related; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    119       Parathyroid hormone.
SQ   SEQUENCE   119 AA;  13943 MW;  B309D8E772997F6E CRC64;

  Query Match             53.1%;  Score 85;  DB 1;  Length 119;
  Best Local Similarity   54.8%;  Pred. No. 0.0027;
  Matches   17;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||:||||  |   :::|| :||: |||||
Db         32 SVSEMQLMHNLGEHRHTVERQDWLQMKLQDV 62


RESULT 13
Q6W9J4_FUGRU
ID   Q6W9J4_FUGRU PRELIMINARY;      PRT;    91 AA.
AC   Q6W9J4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Parathyroid hormone type-2.
GN   Name=PTH;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14684608; DOI=10.1210/en.2003-0964;
RA   Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
RA   Bastepe M., Rubin D.A., Juppner H.;
RT   "Identification and characterization of two parathyroid hormone-like
RT   molecules in zebrafish.";
RL   Endocrinology 145:1634-1639(2004).
DR   EMBL; AY302221; AAQ73561.1; -; Genomic_DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   GO; GO:0007595; P:lactation; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   InterPro; IPR003626; PTH_related.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   ProDom; PD013225; PTH_related; 2.
DR   SMART; SM00087; PTH; 1.
SQ   SEQUENCE   91 AA;  10647 MW;  75BBA25CEA64BF68 CRC64;

  Query Match             42.5%;  Score 68;  DB 2;  Length 91;
  Best Local Similarity   46.7%;  Pred. No. 0.38;
  Matches   14;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||:||||          || :||::||:||
Db         31 ISEVQLMHNVREHKQVGERQDWLQEKLKDV 60


RESULT 14
CB30_HYDMC
ID   CB30_HYDMC     STANDARD;      PRT;    15 AA.
AC   P83630;
DT   25-OCT-2004 (Rel. 45, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Chitin-binding protein HM30 (Fragment).
OS   Hydrangea macrophylla (Bigleaf hydrangea).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   asterids; Cornales; Hydrangeaceae; Hydrangea.
OX   NCBI_TaxID=23110;
RN   [1]
RP   PROTEIN SEQUENCE, FUNCTION, INDUCTION, AND MASS SPECTROMETRY.
RC   TISSUE=Leaf;
RX   MEDLINE=21671918; PubMed=11812226; DOI=10.1006/prep.2001.1551;
RA   Yang Q., Gong Z.-Z.;
RT   "Purification and characterization of an ethylene-induced antifungal
RT   protein from leaves of Guilder rose (Hydrangea macrophylla).";
RL   Protein Expr. Purif. 24:76-82(2002).
CC   -!- FUNCTION: Has antifungal activity against A.alternate,
CC       A.cucumerina, A.niger, C.gossypii, F.oxysporum, F.oxysporum subsp
CC       melonis, F.moniliforme, T.cucumeris, and V.dahliae. Has no
CC       chitinase or agglutination activities.
CC   -!- INDUCTION: By ethylene.
CC   -!- MASS SPECTROMETRY: MW=30010; METHOD=Electrospray; RANGE=1-?;
CC       NOTE=Ref.1.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   -!- CAUTION: 14 of the 15 residues are identical to an internal region
CC       of human parathyroid hormone. That seems quite an incredible
CC       "coincidence".
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
KW   Antimicrobial; Chitin-binding; Direct protein sequencing; Fungicide.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1875 MW;  7EE51EEC7D5B84DD CRC64;

  Query Match             40.6%;  Score 65;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 0.15;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 NSMERVEWLRKKLQD 30
              ||||||| |||||||
Db          1 NSMERVEELRKKLQD 15
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RESULT 15
Q9I8E9_FUGRU
ID   Q9I8E9_FUGRU PRELIMINARY;      PRT;   163 AA.
AC   Q9I8E9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Parathyroid hormone-related protein precursor.
GN   Name=PTHrP;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20314478; PubMed=10854780; DOI=10.1016/S0378-1119(00)00167-0;
RA   Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
RA   Elgar G., Clark M.S.;
RT   "Genomic structure and expression of parathyroid hormone-related
RT   protein in a teleost, Fugu rubripes.";
RL   Gene 250:67-76(2000).
DR   EMBL; AJ249391; CAB94712.1; -; Genomic_DNA.
DR   HSSP; P12272; 1BZG.
DR   Ensembl; SINFRUG00000131728; Fugu rubripes.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   GO; GO:0007595; P:lactation; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003626; PTH_related.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD013225; PTH_related; 1.
KW   Signal.
FT   SIGNAL       1     34       Potential.
SQ   SEQUENCE   163 AA;  18698 MW;  3AC5F2C764732278 CRC64;

  Query Match             40.6%;  Score 65;  DB 2;  Length 163;
  Best Local Similarity   45.2%;  Pred. No. 1.7;
  Matches   14;  Conservative    3;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||  ||||  |  |     |  || | |::|
Db         38 SVSHAQLMHDKGRSLQEFRRRMWLHKLLEEV 68


Search completed: November 21, 2005, 16:15:11
Job time : 148.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:05:03 ; Search time 33 Seconds
(without alignments)
77.665 Million cell updates/sec

Title: US-09-475-158A-3
Perfect score: 160
Sequence: 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	129	80.6	35	1	US-08-142-551B-46	Sequence 46, Appl
2	128	80.0	33	2	US-09-447-800-6	Sequence 6, Appli
3	128	80.0	34	2	US-09-447-800-5	Sequence 5, Appli
4	127	79.4	34	2	US-09-044-536A-12	Sequence 12, Appl
5	127	79.4	34	2	US-09-843-221A-17	Sequence 17, Appl
6	127	79.4	34	2	US-09-843-221A-18	Sequence 18, Appl
7	127	79.4	34	2	US-09-843-221A-162	Sequence 162, App
8	127	79.4	34	2	US-09-843-221A-163	Sequence 163, App
9	127	79.4	35	1	US-08-142-551B-52	Sequence 52, Appl
10	127	79.4	35	1	US-08-142-551B-56	Sequence 56, Appl
11	126	78.8	34	2	US-09-044-536A-8	Sequence 8, Appli
12	125	78.1	31	1	US-08-262-495C-3	Sequence 3, Appli
13	125	78.1	31	1	US-08-691-647C-1	Sequence 1, Appli
14	125	78.1	31	1	US-08-691-647C-6	Sequence 6, Appli
15	125	78.1	31	2	US-08-904-760B-1	Sequence 1, Appli
16	125	78.1	31	2	US-08-904-760B-6	Sequence 6, Appli
17	125	78.1	31	2	US-08-904-760B-14	Sequence 14, Appl
18	125	78.1	31	2	US-08-904-760B-32	Sequence 32, Appl
19	125	78.1	31	2	US-09-406-813-2	Sequence 2, Appli
20	125	78.1	31	2	US-09-536-785A-1	Sequence 1, Appli
21	125	78.1	31	2	US-09-536-785A-6	Sequence 6, Appli
22	125	78.1	31	2	US-09-536-785A-14	Sequence 14, Appl
23	125	78.1	31	2	US-09-536-785A-32	Sequence 32, Appl
24	125	78.1	31	2	US-09-843-221A-27	Sequence 27, Appl
25	125	78.1	31	2	US-09-843-221A-165	Sequence 165, App
26	125	78.1	31	2	US-09-623-548A-271	Sequence 271, App
27	125	78.1	31	2	US-09-657-276-271	Sequence 271, App
28	125	78.1	33	2	US-09-447-800-9	Sequence 9, Appli
29	125	78.1	34	1	US-07-765-373-1	Sequence 1, Appli
30	125	78.1	34	1	US-08-033-099-1	Sequence 1, Appli
31	125	78.1	34	1	US-08-262-495C-1	Sequence 1, Appli
32	125	78.1	34	1	US-07-915-247A-1	Sequence 1, Appli
33	125	78.1	34	1	US-08-443-863-1	Sequence 1, Appli
34	125	78.1	34	1	US-08-448-070-1	Sequence 1, Appli
35	125	78.1	34	1	US-08-488-105-7	Sequence 7, Appli
36	125	78.1	34	1	US-08-468-275-6	Sequence 6, Appli
37	125	78.1	34	1	US-08-449-500-1	Sequence 1, Appli
38	125	78.1	34	1	US-08-449-317A-1	Sequence 1, Appli
39	125	78.1	34	1	US-08-142-551B-2	Sequence 2, Appli
40	125	78.1	34	1	US-08-477-022-1	Sequence 1, Appli
41	125	78.1	34	1	US-08-449-447-1	Sequence 1, Appli
42	125	78.1	34	1	US-08-835-231-13	Sequence 13, Appl
43	125	78.1	34	1	US-08-184-328-1	Sequence 1, Appli
44	125	78.1	34	1	US-08-411-726-2	Sequence 2, Appli
45	125	78.1	34	1	US-08-691-647C-5	Sequence 5, Appli

ALIGNMENTS

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RESULT 1
US-08-142-551B-46
; Sequence 46, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
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;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-46

  Query Match             80.6%;  Score 129;  DB 1;  Length 35;
  Best Local Similarity   80.6%;  Pred. No. 5.8e-10;
  Matches   25;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :||||||:| ||  |||:|||||||||||||
Db          1 SVSEIQLLHNGGKHLNSLERVEWLRKKLQDV 31


RESULT 2
US-09-447-800-6
; Sequence 6, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION: ANALOGS
;  FILE REFERENCE: 0609.4630001
;  CURRENT APPLICATION NUMBER: US/09/447,800
;  CURRENT FILING DATE: 1999-11-23
;  EARLIER APPLICATION NUMBER: 60/110,152
;  EARLIER FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-09-447-800-6

  Query Match             80.0%;  Score 128;  DB 2;  Length 33;
  Best Local Similarity   87.1%;  Pred. No. 7.3e-10;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 3
US-09-447-800-5
; Sequence 5, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION: ANALOGS
;  FILE REFERENCE: 0609.4630001
;  CURRENT APPLICATION NUMBER: US/09/447,800
;  CURRENT FILING DATE: 1999-11-23
;  EARLIER APPLICATION NUMBER: 60/110,152
;  EARLIER FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-09-447-800-5

  Query Match             80.0%;  Score 128;  DB 2;  Length 34;
  Best Local Similarity   87.1%;  Pred. No. 7.5e-10;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 4
US-09-044-536A-12
; Sequence 12, Application US/09044536A
; Patent No. 6025467
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  NAKAGAWA, Shizue
;    APPLICANT:  HABASHITA, Junko
;    APPLICANT:  TAKETOMI, Shigehisa
;    TITLE OF INVENTION:  PARATHYROID HORMONE DERIVATIVES AND THEIR USE
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/044,536A
;      FILING DATE:  19-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/662,871
;      FILING DATE:  12-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CONLIN, David G
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  46509-DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  partial peptide
;      LOCATION:  1..34
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  /product= "Xaa=Ala(2-Naph)"
US-09-044-536A-12

  Query Match             79.4%;  Score 127;  DB 2;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 1e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||||  |  ||||||||||||||||
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Db          1 SVSEIQLMHDXGKHLNSMERVEWLRKKLQDV 31


RESULT 5
US-09-843-221A-17
; Sequence 17, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-17

  Query Match             79.4%;  Score 127;  DB 2;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 1e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 6
US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-18

  Query Match             79.4%;  Score 127;  DB 2;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 1e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 7
US-09-843-221A-162
; Sequence 162, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162

  Query Match             79.4%;  Score 127;  DB 2;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 1e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 8
US-09-843-221A-163
; Sequence 163, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
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;   OTHER INFORMATION: Preferred embodiments - PTH
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163

  Query Match             79.4%;  Score 127;  DB 2;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 1e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||||  |  ||||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 9
US-08-142-551B-52
; Sequence 52, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-52

  Query Match             79.4%;  Score 127;  DB 1;  Length 35;
  Best Local Similarity   80.6%;  Pred. No. 1e-09;
  Matches   25;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||:|  || |||:||||||||||||||
Db          1 SVSEIQLLHNLGGHLNSLERVEWLRKKLQDV 31


RESULT 10
US-08-142-551B-56
; Sequence 56, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-56

  Query Match             79.4%;  Score 127;  DB 1;  Length 35;
  Best Local Similarity   80.6%;  Pred. No. 1e-09;
  Matches   25;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||:|  | ||||:||||||||||||||
Db          1 SVSEIQLLHNLGKGLNSLERVEWLRKKLQDV 31
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RESULT 11
US-09-044-536A-8
; Sequence 8, Application US/09044536A
; Patent No. 6025467
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  NAKAGAWA, Shizue
;    APPLICANT:  HABASHITA, Junko
;    APPLICANT:  TAKETOMI, Shigehisa
;    TITLE OF INVENTION:  PARATHYROID HORMONE DERIVATIVES AND THEIR USE
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/044,536A
;      FILING DATE:  19-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/662,871
;      FILING DATE:  12-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CONLIN, David G
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  46509-DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  partial peptide
;      LOCATION:  1..34
US-09-044-536A-8

  Query Match             78.8%;  Score 126;  DB 2;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 1.4e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| | ||||||||||||||||||
Db          1 SVSEIQLMHDKGKHLNSMERVEWLRKKLQDV 31


RESULT 12
US-08-262-495C-3
; Sequence 3, Application US/08262495C
; Patent No. 5556940
;  GENERAL INFORMATION:
;    APPLICANT:  WILLICK, Gordon E.
;    APPLICANT:  WHITFIELD, James F.
;    APPLICANT:  SUREWICZ, Witold
;    APPLICANT:  SUNG, Wing L.
;    APPLICANT:  NEUGENBAUER, Witold
;    TITLE OF INVENTION:  PARATHYROID HORMONE ANALOGUES
;    TITLE OF INVENTION:  FOR THE TREATMENT OF OSTEOPOROSIS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kirby, Eades, Gale, Baker
;      STREET:  112 Kent Street, Suite 770,
;      CITY:  Ottawa
;      COUNTRY:  Canada
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/262,495C
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  EADES, No. 5556940ris M.
;      REGISTRATION NUMBER:  5,263
;      REFERENCE/DOCKET NUMBER:  36210
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613)-237-6900
;      TELEFAX:  (613)-237-0045
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-262-495C-3

  Query Match             78.1%;  Score 125;  DB 1;  Length 31;
  Best Local Similarity   83.9%;  Pred. No. 1.7e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| | ||||||||||||||||||
Db          1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 13
US-08-691-647C-1
; Sequence 1, Application US/08691647C
; Patent No. 5955425
;  GENERAL INFORMATION:
;    APPLICANT:  Barbier, Jean-Rene
;    APPLICANT:  Morley, Paul
;    APPLICANT:  Neugebauer, Witold
;    APPLICANT:  Ross, Virginia
;    APPLICANT:  Whitfield, James
;    APPLICANT:  Willick, Gordon E.
;    TITLE OF INVENTION:  CYCLIC PARATHYROID HORMONE ANALOGUES
;    TITLE OF INVENTION:  FOR THE TREATMENT OF OSTEOPOROSIS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE, P.C.
;      STREET:  1100 New York Avenue, 8th Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/691,647C
;      FILING DATE:  August 2, 1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Crawford, Arthur R.
;      REGISTRATION NUMBER:  25,327
```

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;      REFERENCE/DOCKET NUMBER:  1339-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 816-4005
;      TELEFAX:  (703) 816-4100
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-691-647C-1

  Query Match             78.1%;  Score 125;  DB 1;  Length 31;
  Best Local Similarity   83.9%;  Pred. No. 1.7e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 14
US-08-691-647C-6
; Sequence 6, Application US/08691647C
; Patent No. 5955425
;  GENERAL INFORMATION:
;    APPLICANT:  Barbier, Jean-Rene
;    APPLICANT:  Morley, Paul
;    APPLICANT:  Neugebauer, Witold
;    APPLICANT:  Ross, Virginia
;    APPLICANT:  Whitfield, James
;    APPLICANT:  Willick, Gordon E.
;    TITLE OF INVENTION:  CYCLIC PARATHYROID HORMONE ANALOGUES
;    TITLE OF INVENTION:  FOR THE TREATMENT OF OSTEOPOROSIS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE, P.C.
;      STREET:  1100 New York Avenue, 8th Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/691,647C
;      FILING DATE:  August 2, 1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Crawford, Arthur R.
;      REGISTRATION NUMBER:  25,327
;      REFERENCE/DOCKET NUMBER:  1339-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 816-4005
;      TELEFAX:  (703) 816-4100
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  cyclic
;    MOLECULE TYPE:  protein
US-08-691-647C-6

  Query Match             78.1%;  Score 125;  DB 1;  Length 31;
  Best Local Similarity   83.9%;  Pred. No. 1.7e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 15
US-08-904-760B-1
; Sequence 1, Application US/08904760B
; Patent No. 6110892
;  GENERAL INFORMATION:
;    APPLICANT:  Jean-Rene, Barbier
;    APPLICANT:  Neugebauer, Witold
;    APPLICANT:  Ross, Virginia
;    APPLICANT:  Whitfield, James
;    APPLICANT:  Willick, Gordon E.
;    TITLE OF INVENTION:  PARATHYROID HORMONE ANALOGUES FOR THE
;    TITLE OF INVENTION:  TREATMENT OF OSTEOPOROSIS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 No. 6110892th Glebe Rd.  8th floor
;      CITY:  Arlington
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201-4741
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/904,760B
;      FILING DATE:  01-AUG-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/691,647
;      FILING DATE:  02-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Crawford, Arthur R.
;      REGISTRATION NUMBER:  25,327
;      REFERENCE/DOCKET NUMBER:  1339-6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4000
;      TELEFAX:  703-816-4100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-904-760B-1

  Query Match             78.1%;  Score 125;  DB 2;  Length 31;
  Best Local Similarity   83.9%;  Pred. No. 1.7e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


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Job time : 33 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:15:23 ; Search time 110.5 Seconds
(without alignments)
117.219 Million cell updates/sec

Title: US-09-475-158A-3
Perfect score: 160
Sequence: 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	128	80.0	33	4	US-10-361-928-6	Sequence 6, Appli
2	128	80.0	34	4	US-10-361-928-5	Sequence 5, Appli
3	127	79.4	34	3	US-09-843-221A-17	Sequence 17, Appl
4	127	79.4	34	3	US-09-843-221A-18	Sequence 18, Appl
5	127	79.4	34	3	US-09-843-221A-162	Sequence 162, App
6	127	79.4	34	3	US-09-843-221A-163	Sequence 163, App
7	127	79.4	34	3	US-09-999-608-17	Sequence 17, Appl
8	127	79.4	34	3	US-09-999-608-18	Sequence 18, Appl
9	127	79.4	34	3	US-09-999-608-162	Sequence 162, App
10	127	79.4	34	3	US-09-999-608-163	Sequence 163, App
11	127	79.4	34	4	US-10-839-037-17	Sequence 17, Appl
12	127	79.4	34	4	US-10-839-037-18	Sequence 18, Appl
13	127	79.4	34	4	US-10-839-037-162	Sequence 162, App
14	127	79.4	34	4	US-10-839-037-163	Sequence 163, App
15	126	78.8	31	5	US-10-892-025-21	Sequence 21, Appl
16	126	78.8	31	5	US-10-892-025-22	Sequence 22, Appl
17	125	78.1	31	3	US-09-169-786-2	Sequence 2, Appli
18	125	78.1	31	3	US-09-843-221A-27	Sequence 27, Appl
19	125	78.1	31	3	US-09-843-221A-165	Sequence 165, App
20	125	78.1	31	3	US-09-999-608-27	Sequence 27, Appl
21	125	78.1	31	3	US-09-999-608-165	Sequence 165, App
22	125	78.1	31	4	US-10-440-473-2	Sequence 2, Appli
23	125	78.1	31	4	US-10-839-037-27	Sequence 27, Appl
24	125	78.1	31	4	US-10-839-037-165	Sequence 165, App
25	125	78.1	31	5	US-10-892-025-1	Sequence 1, Appli
26	125	78.1	31	6	US-11-066-697-271	Sequence 271, App
27	125	78.1	31	6	US-11-040-557-2	Sequence 2, Appli
28	125	78.1	32	5	US-10-892-025-2	Sequence 2, Appli
29	125	78.1	32	6	US-11-040-557-20	Sequence 20, Appl
30	125	78.1	33	4	US-10-361-928-9	Sequence 9, Appli
31	125	78.1	33	5	US-10-892-025-3	Sequence 3, Appli
32	125	78.1	33	6	US-11-040-557-1	Sequence 1, Appli
33	125	78.1	33	6	US-11-040-557-21	Sequence 21, Appl
34	125	78.1	34	3	US-09-169-786-3	Sequence 3, Appli
35	125	78.1	34	3	US-09-858-880-5	Sequence 5, Appli
36	125	78.1	34	3	US-09-928-047B-6	Sequence 6, Appli
37	125	78.1	34	3	US-09-843-221A-16	Sequence 16, Appl
38	125	78.1	34	3	US-09-843-221A-161	Sequence 161, App
39	125	78.1	34	3	US-09-928-048A-6	Sequence 6, Appli
40	125	78.1	34	3	US-09-999-608-16	Sequence 16, Appl
41	125	78.1	34	3	US-09-999-608-161	Sequence 161, App
42	125	78.1	34	3	US-09-999-608-174	Sequence 174, App
43	125	78.1	34	3	US-09-999-608-175	Sequence 175, App
44	125	78.1	34	3	US-09-999-608-193	Sequence 193, App
45	125	78.1	34	4	US-10-016-403-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-361-928-6
; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-6

Query Match 80.0%; Score 128; DB 4; Length 33;
Best Local Similarity 87.1%; Pred. No. 2e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
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RESULT 2
US-10-361-928-5
; Sequence 5, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928

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;  CURRENT FILING DATE:  2003-02-11
;  PRIOR APPLICATION NUMBER: 09/447,800
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: 60/110,152
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-10-361-928-5

  Query Match             80.0%;  Score 128;  DB 4;  Length 34;
  Best Local Similarity   87.1%;  Pred. No. 2.1e-09;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||  |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 3
US-09-843-221A-17
; Sequence 17, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-17

  Query Match             79.4%;  Score 127;  DB 3;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||||  |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 4
US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-18

  Query Match             79.4%;  Score 127;  DB 3;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||||  |  ||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 5
US-09-843-221A-162
; Sequence 162, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HO
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162

  Query Match             79.4%;  Score 127;  DB 3;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||||  |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 6
US-09-843-221A-163
; Sequence 163, Application US/09843221A
```

```
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163

  Query Match             79.4%;  Score 127;  DB 3;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| | ||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 7
US-09-999-608-17
; Sequence 17, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  GEGG, COLIN V.
;  APPLICANT:  JAROSINSKI, MARK ANTHONY
;  APPLICANT:  KINSTLER, OLAF BORIS
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
;  TITLE OF INVENTION:  HORMONE-RELATED PROTEIN
;  FILE REFERENCE: A-665C
;  CURRENT APPLICATION NUMBER: US/09/999,608
;  CURRENT FILING DATE:  2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/843,221
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: US 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: US 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modifiied human PTH
US-09-999-608-17

  Query Match             79.4%;  Score 127;  DB 3;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| | ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 8
US-09-999-608-18
; Sequence 18, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  GEGG, COLIN V.
;  APPLICANT:  JAROSINSKI, MARK ANTHONY
;  APPLICANT:  KINSTLER, OLAF BORIS
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
;  TITLE OF INVENTION:  HORMONE-RELATED PROTEIN
;  FILE REFERENCE: A-665C
;  CURRENT APPLICATION NUMBER: US/09/999,608
;  CURRENT FILING DATE:  2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/843,221
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: US 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: US 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-999-608-18

  Query Match             79.4%;  Score 127;  DB 3;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| | ||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 9
US-09-999-608-162
; Sequence 162, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  GEGG, COLIN V.
;  APPLICANT:  JAROSINSKI, MARK ANTHONY
;  APPLICANT:  KINSTLER, OLAF BORIS
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
;  TITLE OF INVENTION:  HORMONE-RELATED PROTEIN
;  FILE REFERENCE: A-665C
;  CURRENT APPLICATION NUMBER: US/09/999,608
;  CURRENT FILING DATE:  2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/843,221
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: US 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: US 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162
;   LENGTH: 34
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-999-608-162

  Query Match             79.4%;  Score 127;  DB 3;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 10
US-09-999-608-163
; Sequence 163, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  GEGG, COLIN V.
;  APPLICANT:  JAROSINSKI, MARK ANTHONY
;  APPLICANT:  KINSTLER, OLAF BORIS
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
;  TITLE OF INVENTION:  HORMONE-RELATED PROTEIN
;  FILE REFERENCE: A-665C
;  CURRENT APPLICATION NUMBER: US/09/999,608
;  CURRENT FILING DATE:  2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/843,221
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: US 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: US 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-999-608-163

  Query Match             79.4%;  Score 127;  DB 3;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 11
US-10-839-037-17
; Sequence 17, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/10/839,037
;  CURRENT FILING DATE:  2004-05-04
;  PRIOR APPLICATION NUMBER: US/09/843,221A
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-10-839-037-17

  Query Match             79.4%;  Score 127;  DB 4;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 12
US-10-839-037-18
; Sequence 18, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HC
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/10/839,037
;  CURRENT FILING DATE:  2004-05-04
;  PRIOR APPLICATION NUMBER: US/09/843,221A
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-10-839-037-18

  Query Match             79.4%;  Score 127;  DB 4;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 13
US-10-839-037-162
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; Sequence 162, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/10/839,037
;  CURRENT FILING DATE:  2004-05-04
;  PRIOR APPLICATION NUMBER: US/09/843,221A
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-10-839-037-162

  Query Match             79.4%;  Score 127;  DB 4;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 14
US-10-839-037-163
; Sequence 163, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/10/839,037
;  CURRENT FILING DATE:  2004-05-04
;  PRIOR APPLICATION NUMBER: US/09/843,221A
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-10-839-037-163

  Query Match             79.4%;  Score 127;  DB 4;  Length 34;
  Best Local Similarity   83.9%;  Pred. No. 2.8e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 15
US-10-892-025-21
; Sequence 21, Application US/10892025
; Publication No. US20050065071A1
; GENERAL INFORMATION:
;  APPLICANT: Morley, Paul
;  APPLICANT:  Whitfield, James F
;  TITLE OF INVENTION: CYCLIC ANALOGS OF HUMAN PARATHYROID
;  TITLE OF INVENTION:  HORMONE FOR THE TREATMENT OF CONDITIONS CHARACTERIZED BY
;  TITLE OF INVENTION:  HYPERPROLIFERATIVE SKIN CELLS
;  FILE REFERENCE: 3583.1000-001
;  CURRENT APPLICATION NUMBER: US/10/892,025
;  CURRENT FILING DATE:  2004-07-15
;  PRIOR APPLICATION NUMBER: 60/487,513
;  PRIOR FILING DATE: 2003-07-15
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 1
;   OTHER INFORMATION: NHR; where R is hydrogen or a linear or branched
;   OTHER INFORMATION: chain alkyl, acyl or aryl group
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 13
;   OTHER INFORMATION: is selected from the group consisting of Lys, Orn,
;   OTHER INFORMATION: Glu, Asp, Cys, and homocysteine
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 31
;   OTHER INFORMATION: Y; where Y is X, His-X, His-Asn-X, or
;   OTHER INFORMATION: His-Asn-Phe-X; X is OR or NHR; and R is hydrogen
;   OTHER INFORMATION: or a linear or branched chain alkyl, acyl or aryl
;   OTHER INFORMATION: group
US-10-892-025-21

  Query Match             78.8%;  Score 126;  DB 5;  Length 31;
  Best Local Similarity   83.9%;  Pred. No. 3.5e-09;
  Matches   26;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
              :|||||||| |  ||||||||||||||||
Db          1 SVSEIQLMHNLGXHLNSMERVEWLRKKLQDV 31


Search completed: November 21, 2005, 16:34:42
Job time : 111.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:16:29 ; Search time 4 Seconds
(without alignments)
8.756 Million cell updates/sec

Title: US-09-475-158A-3
Perfect score: 160
Sequence: 1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	29.4	263	1	US-10-512-184-29	Sequence 29, Appl
2	46.5	29.1	317	7	US-11-082-389-28	Sequence 28, Appl
3	44	27.5	157	1	US-10-957-569-64	Sequence 64, Appl
4	44	27.5	1213	7	US-11-074-176-256	Sequence 256, App
5	44	27.5	1493	7	US-11-004-057-21	Sequence 21, Appl
6	42	26.2	28	1	US-10-939-890-474	Sequence 474, App
7	42	26.2	28	1	US-10-939-890-726	Sequence 726, App
8	40	25.0	28	1	US-10-939-890-464	Sequence 464, App
9	40	25.0	28	1	US-10-939-890-720	Sequence 720, App
10	40	25.0	28	1	US-10-939-890-723	Sequence 723, App
11	40	25.0	1493	7	US-11-004-057-4	Sequence 4, Appli
12	39	24.4	120	7	US-11-077-978-7	Sequence 7, Appli
13	39	24.4	360	7	US-11-084-408-3	Sequence 3, Appli
14	39	24.4	386	1	US-10-131-826A-340	Sequence 340, App
15	39	24.4	562	7	US-11-065-943-20	Sequence 20, Appl
16	39	24.4	562	7	US-11-065-943-22	Sequence 22, Appl
17	39	24.4	562	7	US-11-065-943-24	Sequence 24, Appl
18	39	24.4	562	7	US-11-065-943-26	Sequence 26, Appl
19	39	24.4	562	7	US-11-065-943-28	Sequence 28, Appl
20	39	24.4	562	7	US-11-065-943-30	Sequence 30, Appl
21	39	24.4	562	7	US-11-065-943-32	Sequence 32, Appl
22	39	24.4	562	7	US-11-065-943-34	Sequence 34, Appl
23	39	24.4	562	7	US-11-065-943-36	Sequence 36, Appl
24	39	24.4	562	7	US-11-065-943-38	Sequence 38, Appl
25	38.5	24.1	346	1	US-10-967-648A-10	Sequence 10, Appl
26	38	23.8	121	1	US-10-789-273-9	Sequence 9, Appli
27	38	23.8	384	7	US-11-074-176-78	Sequence 78, Appl
28	38	23.8	429	1	US-10-131-826A-94	Sequence 94, Appl
29	38	23.8	828	1	US-10-467-962B-99	Sequence 99, Appl
30	37.5	23.4	138	1	US-10-789-273-4	Sequence 4, Appli
31	37	23.1	98	1	US-10-789-273-10	Sequence 10, Appl
32	37	23.1	98	7	US-11-144-248-32	Sequence 32, Appl
33	37	23.1	102	1	US-10-997-201A-6	Sequence 6, Appli
34	37	23.1	121	7	US-11-077-978-2	Sequence 2, Appli
35	37	23.1	121	7	US-11-077-978-3	Sequence 3, Appli
36	37	23.1	122	7	US-11-144-248-24	Sequence 24, Appl
37	37	23.1	125	7	US-11-144-248-16	Sequence 16, Appl
38	37	23.1	138	1	US-10-789-273-8	Sequence 8, Appli
39	37	23.1	138	1	US-10-789-273-12	Sequence 12, Appl
40	37	23.1	139	1	US-10-721-763-33	Sequence 33, Appl
41	37	23.1	401	1	US-10-510-386-68	Sequence 68, Appl
42	37	23.1	470	7	US-11-144-248-45	Sequence 45, Appl
43	37	23.1	470	7	US-11-144-248-46	Sequence 46, Appl
44	36.5	22.8	114	1	US-10-972-587-37	Sequence 37, Appl
45	36.5	22.8	336	1	US-10-499-715-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-512-184-29
; Sequence 29, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SPIII7
; OTHER INFORMATION: with specificity against Fusarium ssp.; originates
; OTHER INFORMATION: from Mus musculus.
US-10-512-184-29

Query Match 29.4%; Score 47; DB 1; Length 263;
Best Local Similarity 29.3%; Pred. No. 2;
Matches 12; Conservative 9; Mismatches 4; Indels 16; Gaps 2;

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Qy          2 VSEIQLMHGGGGGL---NSME------------RVEWLRK 26
              ::|:||:  ||| :   ||::            |: |||:
Db          1 MAEVQLVESGGGLVRPGNSLKLSCVTSGFTFSNYRMHWLRQ 41
```

RESULT 2
US-11-082-389-28
; Sequence 28, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389

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;  CURRENT FILING DATE:  2005-03-16
;  PRIOR APPLICATION NUMBER: US 09/603024
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: US 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 60/143262
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: US 60/151281
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19930487.4
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: DE 19930489.0
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: DE 19931549.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931550.7
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932134.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19941379.7
;  PRIOR FILING DATE: 1999-08-31
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 28
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-11-082-389-28

  Query Match             29.1%;  Score 46.5;  DB 7;  Length 317;
  Best Local Similarity   41.4%;  Pred. No. 2.8;
  Matches   12;  Conservative    4;  Mismatches    8;  Indels    5;  Gaps    1;

Qy          2 VSEIQLMHGGGGGLNSMERVEWLRKKLQD 30
              |||  ::  |||| :|     ||   |:|
Db         86 VSEADIIIVGGGGYDS-----WLYGTLED 109


RESULT 3
US-10-957-569-64
; Sequence 64, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
;  APPLICANT: COOK, Zhihong et al.
;  TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2750-1577PUS3
;  CURRENT APPLICATION NUMBER: US/10/957,569
;  CURRENT FILING DATE:  2004-09-30
;  PRIOR APPLICATION NUMBER: US 10/950,321
;  PRIOR FILING DATE: 2004-09-23
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-957-569-64

  Query Match             27.5%;  Score 44;  DB 1;  Length 157;
  Best Local Similarity   50.0%;  Pred. No. 2.9;
  Matches    8;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         10 GGGGGLNSMERVEWLR 25
              ||||| :|    :| |
Db         88 GGGGGSSSSRSRDWKR 103


RESULT 4
US-11-074-176-256
; Sequence 256, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
;  APPLICANT: Klaenhammer, Todd R.
;  APPLICANT:  Russell, William M.
;  APPLICANT:  Altermann, Eric
;  APPLICANT:  McAuliffe, Olivia
;  APPLICANT:  Peril, Andrea Azcarate
;  TITLE OF INVENTION: Nucleic Acid Sequences Encoding
;  TITLE OF INVENTION:  Stress-Related Proteins and Uses Therefore
;  FILE REFERENCE: 5051-694
;  CURRENT APPLICATION NUMBER: US/11/074,176
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: 60/551,161
;  PRIOR FILING DATE: 2004-03-08
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 256
;   LENGTH: 1213
;   TYPE: PRT
;   ORGANISM: Lactobacillus acidophilus
US-11-074-176-256

  Query Match             27.5%;  Score 44;  DB 7;  Length 1213;
  Best Local Similarity   25.6%;  Pred. No. 26;
  Matches   11;  Conservative    8;  Mismatches    6;  Indels   18;  Gaps    1;

Qy          3 SEIQLMHGGGG-----------------GLNSMERVEWLRKK 27
              : ::: |||||                 |:|:| ||   :|:
Db        873 TSLRVPHGGGGIVQDVKVYTREAGDELSPGVNTMVRVYIAQKR 915


RESULT 5
US-11-004-057-21
; Sequence 21, Application US/11004057
; Publication No. US20050244846A1
; GENERAL INFORMATION:
;  APPLICANT: Johnson, Gary L.
;  TITLE OF INVENTION: MEKK1 PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING
;  TITLE OF INVENTION:  APOPTOSIS
;  FILE REFERENCE: CPI-042CPPC
;  CURRENT APPLICATION NUMBER: US/11/004,057
;  CURRENT FILING DATE:  2004-12-02
;  PRIOR APPLICATION NUMBER: US/09/403,075
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 1493
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-11-004-057-21

  Query Match             27.5%;  Score 44;  DB 7;  Length 1493;
  Best Local Similarity   27.5%;  Pred. No. 32;
  Matches   11;  Conservative    4;  Mismatches    7;  Indels   18;  Gaps    1;

Qy         10 GGGGGLN-----------------SMERVEWLRKKLQDV 31
              |||| |                  || :| |::|: |
Db         26 GGGGALQGSGAPAAGAGLLRETGSAGRERADWRRQQLRKV 65


RESULT 6
US-10-939-890-474
; Sequence 474, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
```

; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-474

Query Match 26.2%; Score 42; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LMHGGGGG 14
::||||||
Db 20 ILHGGGGG 27

RESULT 7
US-10-939-890-726
; Sequence 726, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 726
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-726

Query Match 26.2%; Score 42; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LMHGGGGG 14
::||||||
Db 20 ILHGGGGG 27

RESULT 8
US-10-939-890-464
; Sequence 464, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01

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;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 464
;    LENGTH: 28
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Library Isolate
US-10-939-890-464

  Query Match             25.0%;  Score 40;  DB 1;  Length 28;
  Best Local Similarity   57.1%;  Pred. No. 1.6;
  Matches    8;  Conservative    3;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          3 SEIQLMH--GGGGG 14
              :::|| |  |||||
Db         14 ADLQLSHFAGGGGG 27


RESULT 9
US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 720
;    LENGTH: 28
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic peptide
;    FEATURE:
;    NAME/KEY: MOD_RES
;    LOCATION: (1)..(1)
;    OTHER INFORMATION: ACETYLATION
;    FEATURE:
;    NAME/KEY: MOD_RES
;    LOCATION: (28)..(28)
;    OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-720

  Query Match             25.0%;  Score 40;  DB 1;  Length 28;
  Best Local Similarity   57.1%;  Pred. No. 1.6;
  Matches    8;  Conservative    3;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          3 SEIQLMH--GGGGG 14
              :::|| |  |||||
Db         14 ADLQLSHFAGGGGG 27


RESULT 10
US-10-939-890-723
; Sequence 723, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 723
;    LENGTH: 28
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic peptide
;    FEATURE:
;    NAME/KEY: MOD_RES
;    LOCATION: (1)..(1)
;    OTHER INFORMATION: ACETYLATION
;    FEATURE:
;    NAME/KEY: MOD_RES
;    LOCATION: (28)..(28)
;    OTHER INFORMATION: Lys residue modifed with a SATA linker
US-10-939-890-723

  Query Match             25.0%;  Score 40;  DB 1;  Length 28;
  Best Local Similarity   57.1%;  Pred. No. 1.6;
  Matches    8;  Conservative    3;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          3 SEIQLMH--GGGGG 14
              :::|| |  |||||
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Db         14 ADLQLSHFAGGGGG 27


RESULT 11
US-11-004-057-4
; Sequence 4, Application US/11004057
; Publication No. US20050244846A1
; GENERAL INFORMATION:
;  APPLICANT: Johnson, Gary L.
;  TITLE OF INVENTION: MEKK1 PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING
;  TITLE OF INVENTION:  APOPTOSIS
;  FILE REFERENCE: CPI-042CPPC
;  CURRENT APPLICATION NUMBER: US/11/004,057
;  CURRENT FILING DATE:  2004-12-02
;  PRIOR APPLICATION NUMBER: US/09/403,075
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1493
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-004-057-4

  Query Match             25.0%;  Score 40;  DB 7;  Length 1493;
  Best Local Similarity   22.7%;  Pred. No. 1.1e+02;
  Matches   10;  Conservative    6;  Mismatches    6;  Indels   22;  Gaps    1;

Qy         10 GGGGGLNSM----------------------ERVEWLRKKLQDV 31
              |||||  ::                      || :| |: :: |
Db         26 GGGGGGGALQGSGAPAAGAAGLLREPGSAGRERADWRRRHVRKV 69


RESULT 12
US-11-077-978-7
; Sequence 7, Application US/11077978
; Publication No. US20050244333A1
; GENERAL INFORMATION:
;  APPLICANT: Yazaki, Paul J.
;  APPLICANT:  Sherman, Mark A.
;  APPLICANT:  Shively, John  E.
;  APPLICANT:  Raubitschek, Andrew A.
;  APPLICANT:  Wu, Anna M.
;  TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
;  FILE REFERENCE: 54435.8012.US01
;  CURRENT APPLICATION NUMBER: US/11/077,978
;  CURRENT FILING DATE:  2005-03-11
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Variable heavy chain of humanized anti-p185HER2 antibody 4D5,
;   OTHER INFORMATION: version 8
US-11-077-978-7

  Query Match             24.4%;  Score 39;  DB 7;  Length 120;
  Best Local Similarity   25.6%;  Pred. No. 10;
  Matches   10;  Conservative    6;  Mismatches    7;  Indels   16;  Gaps    2;

Qy          4 EIQLMHGGGG--------------GLNSMER-VEWLRK 26
              |:||:  |||              | |  :  : |:|:
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ 39


RESULT 13
US-11-084-408-3
; Sequence 3, Application US/11084408
; Publication No. US20050249712A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Lenord, Warren J.
;  APPLICANT:  Pandey, Akhilesh
;  APPLICANT:  Al-Shami, Amin
;  APPLICANT:  Spolski, Rosanne
;  APPLICANT:  Kelly, John
;  APPLICANT:  Keane-Myers, Andrea M.
;  TITLE OF INVENTION: METHODS FOR USE OF TSLP AND AGONISTS AND ANTAGONISTS THEREOF
;  FILE REFERENCE: 4239-67781-02
;  CURRENT APPLICATION NUMBER: US/11/084,408
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US 60/555,898
;  PRIOR FILING DATE: 2004-03-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-11-084-408-3

  Query Match             24.4%;  Score 39;  DB 7;  Length 360;
  Best Local Similarity   38.5%;  Pred. No. 34;
  Matches   10;  Conservative    4;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          4 EIQLMHGGGGGLNSMER--VEWLRKK 27
              |: |  |||  | | ::     ||| :
Db        100 EVVLREGGGAKLFSRKKKASAWLRPR 125


RESULT 14
US-10-131-826A-340
; Sequence 340, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C128
;  CURRENT APPLICATION NUMBER: US/10/131,826A
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
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;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 340
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-131-826A-340

  Query Match             24.4%;  Score 39;  DB 1;  Length 386;
  Best Local Similarity   47.1%;  Pred. No. 36;
  Matches    8;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          10 GGGGGLNSMERVEWLRK 26
               |||||   : || : |:
Db         246 GGGGGPERVHRVLFRRR 262


RESULT 15
US-11-065-943-20
; Sequence 20, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
;  APPLICANT: JESTIN, JEAN-LUC
;  APPLICANT:  VICHIER-GUERRE, SOPHIE
;  APPLICANT:  FERRIS, STEPHANE
;  TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
;  TITLE OF INVENTION:  VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
;  TITLE OF INVENTION:  METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
;  FILE REFERENCE: 266426US0XCIP
;  CURRENT APPLICATION NUMBER: US/11/065,943
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 10/787,219
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Thermus aquaticus
US-11-065-943-20

  Query Match             24.4%;  Score 39;  DB 7;  Length 562;
  Best Local Similarity   42.9%;  Pred. No. 54;
  Matches    6;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          10 GGGGGLNSMERVEW 23
               ||||   ::|   |
Db           9 GGGGSPKALEEAPW 22


Search completed: November 21, 2005, 16:34:56
Job time : 4.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 15:52:37 ; Search time 141.5 Seconds
(without alignments)
96.260 Million cell updates/sec

Title: US-09-475-158A-5
Perfect score: 162
Sequence: 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	162	100.0	31	3	AAY96974	Aay96974 Parathyro
2	127	78.4	31	3	AAY96973	Aay96973 Parathyro
3	116	71.6	31	3	AAY96975	Aay96975 Parathyro
4	104	64.2	89	8	ADG93251	Adg93251 Novel exp
5	103	63.6	84	2	AAR21190	Aar21190 Human par
6	103	63.6	91	8	ADF90346	Adf90346 Chimeric
7	103	63.6	91	8	ADJ87052	Adj87052 Amino aci
8	103	63.6	141	8	ADF90348	Adf90348 Chimeric
9	100	61.7	34	3	ABJ10769	Abj10769 Human par
10	100	61.7	34	3	ABJ10737	Abj10737 Human par
11	100	61.7	38	2	AAR58104	Aar58104 [Gly13]-h
12	100	61.7	38	2	AAR98958	Aar98958 Target pe
13	100	61.7	84	2	AAR21168	Aar21168 Human par
14	99	61.1	84	2	AAR23334	Aar23334 Bovine pa
15	98	60.5	34	2	AAW17939	Aaw17939 Human par
16	98	60.5	34	2	AAW67274	Aaw67274 Parathyro
17	98	60.5	34	3	ABJ10713	Abj10713 Human par
18	98	60.5	35	2	AAR74454	Aar74454 Parathyro
19	98	60.5	35	2	AAR74462	Aar74462 Parathyro
20	98	60.5	35	2	AAR74451	Aar74451 Parathyro
21	98	60.5	84	2	AAR21226	Aar21226 Human par
22	98	60.5	84	2	AAR21240	Aar21240 Human par
23	98	60.5	84	2	AAR21227	Aar21227 Human par
24	97	59.9	84	2	AAR21172	Aar21172 Human par
25	97	59.9	84	2	AAR21178	Aar21178 Human par
26	97	59.9	84	2	AAR21236	Aar21236 Human par
27	97	59.9	84	2	AAR21234	Aar21234 Human par
28	97	59.9	84	2	AAR21235	Aar21235 Human par
29	97	59.9	84	2	AAR21179	Aar21179 Human par
30	96	59.3	34	2	AAR22294	Aar22294 Human par
31	96	59.3	35	2	AAR74457	Aar74457 Parathyro
32	96	59.3	35	2	AAR74466	Aar74466 Parathyro
33	96	59.3	35	2	AAR74470	Aar74470 Parathyro
34	96	59.3	36	2	AAR58271	Aar58271 [Ala11]-h
35	96	59.3	84	2	AAR21233	Aar21233 Human par
36	96	59.3	84	2	AAR21231	Aar21231 Human par
37	96	59.3	84	2	AAR21232	Aar21232 Human par
38	96	59.3	84	2	AAR23312	Aar23312 Bovine pa
39	96	59.3	84	2	AAR21176	Aar21176 Human par
40	95	58.6	33	3	AAY98015	Aay98015 Human ami
41	95	58.6	34	2	AAR49697	Aar49697 Sequence
42	95	58.6	34	2	AAW17943	Aaw17943 Human par
43	95	58.6	34	2	AAW17941	Aaw17941 Human par
44	95	58.6	34	2	AAW67276	Aaw67276 Parathyro
45	95	58.6	34	2	AAW67278	Aaw67278 Parathyro

ALIGNMENTS

RESULT 1
AAY96974
ID AAY96974 standard; peptide; 31 AA.
XX
AC AAY96974;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone functional domain conjugate peptide PG9.
XX
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .5
FT /label= PTH_N-terminal_signaling_domain
FT /note= "residues 1-5"
FT Peptide 6. .14
FT /label= linker
FT Peptide 15. .31
FT /label= PTH_C-terminal_binding_portion
FT /note= "residues 15-31"
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
DR N-PSDB; AAA51731.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.

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XX
PS   Claim 7; Page 93; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 31 AA;

  Query Match             100.0%;  Score 162;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-13;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||||||||||||||||||||||||||||
Db          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31


RESULT 2
AAY96973
ID   AAY96973 standard; peptide; 31 AA.
XX
AC   AAY96973;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Parathyroid hormone functional domain conjugate peptide PG5.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .9
FT                   /label= PTH_N-terminal_signaling_domain
FT                   /note= "residues 1-9"
FT   Peptide         10. .14
FT                   /label= linker
FT   Peptide         15. .30
FT                   /label= PTH_C-terminal_binding_portion
FT                   /note= "residues 15-31"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   N-PSDB; AAA51729.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 7; Page 92-93; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 31 AA;

  Query Match             78.4%;  Score 127;  DB 3;  Length 31;
  Best Local Similarity   87.1%;  Pred. No. 1.7e-08;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||    ||||||||||||||||||||||
Db          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31


RESULT 3
AAY96975
ID   AAY96975 standard; peptide; 31 AA.
XX
AC   AAY96975;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Parathyroid hormone functional domain conjugate peptide PG7.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .9
FT                   /label= PTH_N-terminal_signaling_domain
FT                   /note= "residues 1-9"
FT   Peptide         10. .16
FT                   /label= linker
FT   Peptide         17. .31
FT                   /label= PTH_C-terminal_binding_portion
FT                   /note= "residues 17-31"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
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DR   WPI; 2000-452384/39.
DR   N-PSDB; AAA51730.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 7; Page 93; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 31 AA;

  Query Match             71.6%;  Score 116;  DB 3;  Length 31;
  Best Local Similarity   77.1%;  Pred. No. 3.9e-07;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    8;  Gaps    2;

Qy          1 AVSEI----GGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||    |||||||    |||||||||||||||
Db          1 AVSEIQLMHGGGGGGG----SMERVEWLRKKLQDV 31


RESULT 4
ADG93251
ID   ADG93251 standard; protein; 89 AA.
XX
AC   ADG93251;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel expression cassette encoded amino acid sequence SeqID132.
XX
KW   expression cassette; high yield polypeptide production;
KW   tandem polypeptide; inclusion body.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003100021-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016643.
XX
PR   24-MAY-2002; 2002US-0383370P.
XX
PA   (REST-) RESTORAGEN INC.
PA   (HARL/) HARLEY S.
XX
PI   Harley S,  Williams JA,  Luan P,  Xia Y;
XX
DR   WPI; 2004-035128/03.
DR   N-PSDB; ADG93252.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Example 6; SEQ ID NO 132; 157pp; English.
XX
CC   This invention relates to a novel expression cassette and methods for
CC   high yield production of polypeptides. The cassette comprises an operably
CC   linked nucleic acid sequence, where the expression of the cassette
CC   produces a tandem polypeptide that forms an inclusion body when expressed
CC   in a cell. The expression cassette is useful for producing peptide and
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present sequence is that of
CC   an amino acid sequence encoded by an expression cassette of the
CC   invention.
XX
SQ   Sequence 89 AA;

  Query Match             64.2%;  Score 104;  DB 8;  Length 89;
  Best Local Similarity   59.0%;  Pred. No. 3.3e-05;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels   12;  Gaps    1;

Qy          5 IGGGGGG------------GGGLNSMERVEWLRKKLQDV 31
              :|||||              |  ||||||||||||||||
Db         48 VGGGGGPRSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 86


RESULT 5
AAR21190
ID   AAR21190 standard; protein; 84 AA.
XX
AC   AAR21190;
XX
DT   25-MAR-2003  (revised)
DT   17-JUN-1992  (first entry)
XX
DE   Human parathyroid hormone analogue, [Ala1Gly6]hPTH.
XX
KW   PTH; agonist; antagonist; receptor binding.
XX
OS   Synthetic.
XX
PN   WO9200753-A.
XX
PD   23-JAN-1992.
XX
PF   13-JUL-1990;   90US-00553760.
XX
PR   13-JUL-1990;   90US-00553760.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cohen FA,  Nissenson RA,  Strewler GJ;
XX
DR   WPI; 1992-056643/07.
XX
PT   New modified parathyroid hormone analogues - useful in treating cancer,
PT   osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
XX
PS   Claim 15; Page 64; 86pp; English.
XX
CC   Residues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-+M
CC   (M+ = cation), or -(C=O)NH2. 140 specific peptides derived from human PTH
CC   are given in the specification (AAR21150-256, AAR23226- 3250 + AAR23522-
CC   529). Corresp. peptides created using residues 7-84 of bovine and porcine
CC   PTH are also claimed. All have mutations at positions 3, and/or 6, and/or
CC   9 which result in surface side chains which are useful to modulate
CC   receptor binding and activity. They are useful as agonists and
CC   antagonists in the treatment of condi- tions or diseases involving PTH.
CC   The peptides are pref. prepd. by solid phase synthesis. See also AAR21257
CC   (human generic), AAR21258 (bovine generic) and AAR21259 (porcine
CC   generic). (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 84 AA;

  Query Match             63.6%;  Score 103;  DB 2;  Length 84;
  Best Local Similarity   77.4%;  Pred. No. 4.1e-05;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;
```

```
Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              ||||||     |  ||||||||||||||||
Db          1 AVSEIGLMHNLGKHLNSMERVEWLRKKLQDV 31
```

RESULT 6
ADF90346
ID ADF90346 standard; protein; 91 AA.
XX
AC ADF90346;
XX
DT 26-FEB-2004 (first entry)
XX
DE Chimeric protein SEQ ID NO:19.
XX
KW palladium complex-promoted hydrolytic polypeptide cleavage;
KW Cys-His cleavage site; palladium promoter; chimeric protein;
KW inclusion body.
XX
OS Synthetic.
XX
PN WO2003100015-A2.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-US016468.
XX
PR 24-MAY-2002; 2002US-0383488P.
XX
PA (REST-) RESTORAGEN INC.
XX
PI Seo JS, Strydom D, Holmquist B;
XX
DR WPI; 2004-053266/05.
DR N-PSDB; ADF90345.
XX
PT A palladium complex-promoted hydrolytic polypeptide cleavage process for
PT cleaving the polypeptide at a Cys-His cleavage site, comprises
PT solubilizing the polypeptide in mixture of a palladium promotor dissolved
PT in organic acid solvent.
XX
PS Example 9; SEQ ID NO 19; 56pp; English.
XX
CC The present invention describes a palladium complex-promoted hydrolytic
CC polypeptide cleavage process, which selectively cleaves the polypeptide
CC at a Cys-His cleavage site. The process comprises solubilising the
CC polypeptide in a reaction mixture comprised of a palladium promoter
CC dissolved in a high-concentration organic acid solvent. Also described:
CC (1) a peptide purification process; and (2) a process for producing a
CC peptide. The methods are useful for selectively cleaving the polypeptide
CC at Cys-His cleavage site. The process provides a highly specific,
CC conformationally independent, palladium promoted hydrolytic cleavage of
CC polypeptides, including cleavage of relatively insoluble chimeric
CC proteins in the form of inclusion bodies. The present sequence is used in
CC the exemplification of the present invention.
XX
SQ Sequence 91 AA;

```
  Query Match             63.6%;  Score 103;  DB 8;  Length 91;
  Best Local Similarity   56.1%;  Pred. No. 4.4e-05;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels   14;  Gaps    1;

Qy          5 IGGGGGG--------------GGGLNSMERVEWLRKKLQDV 31
              :|||||               |  ||||||||||||||||
Db         48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88
```

RESULT 7
ADJ87052
ID ADJ87052 standard; protein; 91 AA.
XX
AC ADJ87052;
XX
DT 06-MAY-2004 (first entry)
XX
DE Amino acid sequence of chimeric protein T7tag-Vg-G5pr-CH-pth(1-34).
XX
KW growth hormone releasing factor; GRF; hydrolytic polypeptide cleavage;
KW palladium promoter; formic acid; inclusion body; glucagon like peptide-1;
KW GLP-1; GLP-2; parathyroid hormone; PTH;
KW parathyroid hormone related hormone; adrenocorticotropic hormone; ACTH;
KW enkephalins; endorphin; exendin; amylin; opioid peptide; gaegurin 5;
KW gaegurin 6; brevinin 1; ranatuerin; esculetin;
KW glucose dependent insulinotropic polypeptide; GIP; glucagon; motilin;
KW thymopoietin; thymosin; ubiquitin; serum thymic factor;
KW thymic humoral factor; neurotensin; tuftsin; gastrin; calcitonin;
KW luteinising hormone releasing hormone; pancreatic polypeptide;
KW endothelin; corticotropin releasing factor; neuropeptide Y;
KW atrial naturetic peptide; amylin; galanin; somatostatin;
KW vasoactive intestinal peptide; insulin; chimera.
XX
OS Chimeric.
OS Synthetic.
XX
PN WO2004011599-A2.
XX
PD 05-FEB-2004.
XX
PF 23-MAY-2003; 2003WO-US016647.
XX
PR 24-MAY-2002; 2002US-0383484P.
XX
PA (REST-) RESTORAGEN INC.
XX
PI Seo JS, Holmquist B;
XX
DR WPI; 2004-203533/19.
DR N-PSDB; ADJ87051.
XX
PT Hydrolytic polypeptide cleavage process useful for selectively cleaving
PT the polypeptide at the Cys-His cleavage site, comprises solubilizing the
PT polypeptide in a reaction mixture containing a palladium promoter
PT dissolved in formic acid.
XX
PS Claim 11; Fig 5; 41pp; English.
XX
CC The present sequence represents chimeric protein T7tag-Vg-G5pr-CH-pth(1-
CC 34). The protein comprises parathyroid hormone (PTH). The chimeric
CC protein is used to demonstrate the process of the invention. The
CC specification describes a hydrolytic polypeptide cleavage process which
CC selectively cleaves the polypeptide at the Cys-His cleavage site. The
CC process comprises solubilising the polypeptide in a reaction mixture
CC containing a palladium promoter dissolved in formic acid. The polypeptide
CC is in the form of an inclusion body, and is preferably glucagon like
CC peptide-1 (GLP-1), GLP-2, growth hormone releasing factor (GRF),
CC parathyroid hormone (PTH), parathyroid hormone related hormone,
CC adrenocorticotropic hormone (ACTH), enkephalins, endorphins, exendins,
CC amylins, various opioid peptides, gaegurin 5, gaegurin 6, brevinin 1,
CC ranatuerin 1-9, an esculetin, glucose dependent insulinotropic
CC polypeptide (GIP), glucagon, motilin, thymopoietin, thymosin, ubiquitin,
CC serum thymic factor, thymic humoral factor, neurotensin, tuftsin,
CC gastrin, calcitonin, luteinising hormone releasing hormone, pancreatic
CC polypeptide, endothelin, corticotropin releasing factor, neuropeptide Y,
CC atrial naturetic peptide, amylin, galanin, somatostatins, vasoactive
CC intestinal peptide or insulin. The process is highly specific, and is not
CC affected by the polypeptide sequence or the size of the cleaved peptide
CC product.
XX
SQ Sequence 91 AA;

```
  Query Match             63.6%;  Score 103;  DB 8;  Length 91;
  Best Local Similarity   56.1%;  Pred. No. 4.4e-05;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels   14;  Gaps    1;

Qy          5 IGGGGGG--------------GGGLNSMERVEWLRKKLQDV 31
              :|||||               |  ||||||||||||||||
```

```
Db         48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88


RESULT 8
ADF90348
ID   ADF90348 standard; protein; 141 AA.
XX
AC   ADF90348;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Chimeric protein SEQ ID NO:21.
XX
KW   palladium complex-promoted hydrolytic polypeptide cleavage;
KW   Cys-His cleavage site; palladium promoter; chimeric protein;
KW   inclusion body.
XX
OS   Synthetic.
XX
PN   WO2003100015-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016468.
XX
PR   24-MAY-2002; 2002US-0383488P.
XX
PA   (REST-) RESTORAGEN INC.
XX
PI   Seo JS,  Strydom D,  Holmquist B;
XX
DR   WPI; 2004-053266/05.
DR   N-PSDB; ADF90347.
XX
PT   A palladium complex-promoted hydrolytic polypeptide cleavage process for
PT   cleaving the polypeptide at a Cys-His cleavage site, comprises
PT   solubilizing the polypeptide in mixture of a palladium promotor dissolved
PT   in organic acid solvent.
XX
PS   Example 11; SEQ ID NO 21; 56pp; English.
XX
CC   The present invention describes a palladium complex-promoted hydrolytic
CC   polypeptide cleavage process, which selectively cleaves the polypeptide
CC   at a Cys-His cleavage site. The process comprises solubilising the
CC   polypeptide in a reaction mixture comprised of a palladium promoter
CC   dissolved in a high-concentration organic acid solvent. Also described:
CC   (1) a peptide purification process; and (2) a process for producing a
CC   peptide. The methods are useful for selectively cleaving the polypeptide
CC   at Cys-His cleavage site. The process provides a highly specific,
CC   conformationally independent, palladium promoted hydrolytic cleavage of
CC   polypeptides, including cleavage of relatively insoluble chimeric
CC   proteins in the form of inclusion bodies. The present sequence is used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 141 AA;

  Query Match             63.6%;  Score 103;  DB 8;  Length 141;
  Best Local Similarity   56.1%;  Pred. No. 6.8e-05;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels   14;  Gaps    1;

Qy          5 IGGGGGG--------------GGGLNSMERVEWLRKKLQDV 31
              :|||||                |  ||||||||||||||||
Db         48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88


RESULT 9
ABJ10769
ID   ABJ10769 standard; peptide; 34 AA.
XX
AC   ABJ10769;
XX
DT   02-DEC-2002  (first entry)
XX
DE   Human parathyroid hormone analogue #65.
XX
KW   Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW   PTHrP; analogue; abnormal CNS function; pancreatic function;
KW   mineral metabolism; male infertility; abnormal blood pressure;
KW   hypothalmic disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /label= OTHER
FT                   /note= "OTHER=cyclohexylalanine"
FT   Modified-site   8
FT                   /label= OTHER
FT                   /note= "OTHER=des-Met"
FT   Modified-site   9
FT                   /label= OTHER
FT                   /note= "OTHER=des-His"
FT   Modified-site   10
FT                   /label= OTHER
FT                   /note= "OTHER=des-Asn"
FT   Modified-site   11
FT                   /label= OTHER
FT                   /note= "OTHER=cyclohexylalanine"
FT   Modified-site   34
FT                   /note= "C-terminal amide"
XX
PN   WO9957139-A2.
XX
PD   11-NOV-1999.
XX
PF   03-MAY-1999;   99WO-US009521.
XX
PR   05-MAY-1998;   98US-00072956.
XX
PA   (SCRC ) SOC CONSEILS RECH & APPL SCI.
XX
PI   Chorev M,  Dong ZX,  Rosenblatt M;
XX
DR   WPI; 2000-038790/03.
XX
PT   New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
PT   pancreatic functions, abnormal mineral metabolism and homeostasis, male
PT   infertility, abnormal blood pressure or hypothalmic disease.
XX
PS   Claim 11; Page 39; 49pp; English.
XX
CC   The present invention provides a number of parathyroid hormone (PTH) or
CC   parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
CC   receptor agonists or antagonists and can be used in the treatment of
CC   disorders resulting from altered or excessive action of the PTH2
CC   receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC   divergence from normal mineral metabolism and homeostasis, male
CC   infertility, abnormal blood pressure or a hypothalmic disease. The
CC   present sequence is a peptide analogue of the invention
XX
SQ   Sequence 34 AA;

  Query Match             61.7%;  Score 100;  DB 3;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||
Db          1 SVSEIQXXXXXGKHLNSMERVEWLRKKLQDV 31


RESULT 10
ABJ10737
ID   ABJ10737 standard; peptide; 34 AA.
XX
```

```
AC   ABJ10737;
XX
DT   02-DEC-2002  (first entry)
XX
DE   Human parathyroid hormone analogue #33.
XX
KW   Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW   PTHrP; analogue; abnormal CNS function; pancreatic function;
KW   mineral metabolism; male infertility; abnormal blood pressure;
KW   hypothalmic disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /label= OTHER
FT                   /note= "OTHER=cyclohexylalanine"
FT   Modified-site   8
FT                   /label= OTHER
FT                   /note= "OTHER=des-Met"
FT   Modified-site   11
FT                   /label= OTHER
FT                   /note= "OTHER=cyclohexylalanine"
FT   Modified-site   34
FT                   /note= "C-terminal amide"
XX
PN   WO9957139-A2.
XX
PD   11-NOV-1999.
XX
PF   03-MAY-1999;   99WO-US009521.
XX
PR   05-MAY-1998;   98US-00072956.
XX
PA   (SCRC ) SOC CONSEILS RECH & APPL SCI.
XX
PI   Chorev M,  Dong ZX,  Rosenblatt M;
XX
DR   WPI; 2000-038790/03.
XX
PT   New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
PT   pancreatic functions, abnormal mineral metabolism and homeostasis, male
PT   infertility, abnormal blood pressure or hypothalmic disease.
XX
PS   Claim 11; Page 39; 49pp; English.
XX
CC   The present invention provides a number of parathyroid hormone (PTH) or
CC   parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
CC   receptor agonists or antagonists and can be used in the treatment of
CC   disorders resulting from altered or excessive action of the PTH2
CC   receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC   divergence from normal mineral metabolism and homeostasis, male
CC   infertility, abnormal blood pressure or a hypothalmic disease. The
CC   present sequence is a peptide analogue of the invention
XX
SQ   Sequence 34 AA;

  Query Match             61.7%;  Score 100;  DB 3;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||       |  ||||||||||||||||
Db          1 SVSEIQXXHNXGKHLNSMERVEWLRKKLQDV 31


RESULT 11
AAR58104
ID   AAR58104 standard; peptide; 38 AA.
XX
AC   AAR58104;
XX
DT   20-SEP-1994  (first entry)
XX
DE   [Gly13]-hPTH(1-38)-OH.
XX
KW   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
KW   fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX
OS   Synthetic.
XX
PN   GB2269176-A.
XX
PD   02-FEB-1994.
XX
PF   12-JUL-1993;   93GB-00014384.
XX
PR   15-JUL-1992;   92GB-00015009.
PR   18-DEC-1992;   92GB-00026415.
PR   23-DEC-1992;   92GB-00026859.
PR   23-DEC-1992;   92GB-00026861.
PR   28-JAN-1993;   93GB-00001691.
PR   28-JAN-1993;   93GB-00001692.
PR   14-APR-1993;   93GB-00007673.
PR   19-APR-1993;   93GB-00008033.
XX
PA   (SANO ) SANDOZ LTD.
XX
PI   Lewis I,  Schneider H,  Waelchli R,  Rainer A;
XX
DR   WPI; 1994-018352/03.
XX
PT   New active para-thyroid hormone variants - used for treating or
PT   preventing osteoporosis etc.
XX
PS   Example 101; Page 39; 92pp; English.
XX
CC   This peptide is an example of a highly generic formula covering
CC   parathyroid hormone variants useful for treating or preventing bone
CC   conditions associated with calcium depletion/resorption, in cases where
CC   calcium fixation is required (esp. osteoporosis) or to treat
CC   hypoparathyroidism
XX
SQ   Sequence 38 AA;

  Query Match             61.7%;  Score 100;  DB 2;  Length 38;
  Best Local Similarity   74.2%;  Pred. No. 4.4e-05;
  Matches   23;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||       || ||||||||||||||||
Db          1 SVSEIQLMHNLGGHLNSMERVEWLRKKLQDV 31


RESULT 12
AAR98958
ID   AAR98958 standard; peptide; 38 AA.
XX
AC   AAR98958;
XX
DT   15-JAN-1997  (first entry)
XX
DE   Target peptide (PTH(1-38)) used in fusion protein construct.
XX
KW   Fusion protein construct; isolation; purification;
KW   growth hormone releasing factor; glucagon-like peptide 1;
KW   parathyroid hormone; inclusion body; carbonic anhydrase.
XX
OS   Synthetic.
XX
PN   WO9617942-A1.
XX
PD   13-JUN-1996.
XX
PF   07-DEC-1995;   95WO-US015800.
```

XX
PR 07-DEC-1994; 94US-00350530.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Partridge BE, Stout JS, Henriksen DB, Manning SD, De La Motte RS;
PI Holmquist B, Wagner FW;
XX
DR WPI; 1996-287186/29.
XX
PT Isolation and purificn of peptide(s) from fusion protein constructs -
PT which include a carbonic anhydrase and a variable fused polypeptide.
XX
PS Claim 58; Page 50; 67pp; English.
XX
CC A new method for the isolation and/or purification of a recombinant
CC peptide employs a fusion protein construct (FPC) comprising a carbonic
CC anhydrase and a variable fused polypeptide containing a target peptide.
CC The method comprises precipitating either the FPC or a fragment of the
CC FPC including the carbonic anhydrase. An alternative method of producing
CC the peptide comprises expressing the FPC as part of an inclusion body.
CC The target peptides of the FPC are derived from growth hormone releasing
CC factor (GRF), glucagon-like peptide 1 (GLP1) or parathyroid hormone
CC (PTH). This sequence corresponds to amino acids 1-38 of PTH
XX
SQ Sequence 38 AA;

Query Match 61.7%; Score 100; DB 2; Length 38;
Best Local Similarity 74.2%; Pred. No. 4.4e-05;
Matches 23; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
:||||| | ||||||||||||||||
Db 1 SVSEIGLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 13
AAR21168
ID AAR21168 standard; protein; 84 AA.
XX
AC AAR21168;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1992 (first entry)
XX
DE Human parathyroid hormone analogue, [Gly6]hPTH.
XX
KW PTH; agonist; antagonist; receptor binding.
XX
OS Synthetic.
XX
PN WO9200753-A.
XX
PD 23-JAN-1992.
XX
PF 13-JUL-1990; 90US-00553760.
XX
PR 13-JUL-1990; 90US-00553760.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cohen FA, Nissenson RA, Strewler GJ;
XX
DR WPI; 1992-056643/07.
XX
PT New modified parathyroid hormone analogues - useful in treating cancer,
PT osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
XX
PS Claim 15; Page 64; 86pp; English.
XX
CC Residues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-+M
CC (M+ = cation), or -(C=O)NH2. 140 specific peptides derived from human PTH
CC are given in the specification (AAR21150-256, AAR23226- 3250 + AAR23522-
CC 529). Corresp. peptides created using residues 7-84 of bovine and porcine
CC PTH are also claimed. All have mutations at positions 3, and/or 6, and/or
CC 9 which result in surface side chains which are useful to modulate
CC receptor binding and activity. They are useful as agonists and
CC antagonists in the treatment of condi- tions or diseases involving PTH.
CC The peptides are pref. prepd. by solid phase synthesis. See also AAR21257
CC (human generic), AAR21258 (bovine generic) and AAR21259 (porcine
CC generic). (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 84 AA;

Query Match 61.7%; Score 100; DB 2; Length 84;
Best Local Similarity 74.2%; Pred. No. 9.6e-05;
Matches 23; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
:||||| | ||||||||||||||||
Db 1 SVSEIGLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 14
AAR23334
ID AAR23334 standard; protein; 84 AA.
XX
AC AAR23334;
XX
DT 25-MAR-2003 (revised)
DT 22-JUN-1992 (first entry)
XX
DE Bovine parathyroid hormone analogue, [Gly6]bPTH.
XX
KW PTH; agonist; antagonist; receptor binding.
XX
OS Synthetic.
XX
PN WO9200753-A.
XX
PD 23-JAN-1992.
XX
PF 13-JUL-1990; 90US-00553760.
XX
PR 13-JUL-1990; 90US-00553760.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cohen FA, Nissenson RA, Strewler GJ;
XX
DR WPI; 1992-056643/07.
XX
PT New modified parathyroid hormone analogues - useful in treating cancer,
PT osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
XX
PS Claim 15; Page 64; 86pp; English.
XX
CC Residues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-+M
CC (M+ = cation), or -(C=O)NH2. 142 specific peptides derived from bovine
CC PTH are given in the specification (AAR23251-382, and AAR23540-549).
CC Corresp. peptides created using residues 7-84 of human and porcine PTH
CC are also claimed. All have mutations at positions 3, and/or 6, and/or 9
CC which result in surface side chains which are useful to modulate receptor
CC binding and activity. They are useful as agonists and antagonists in the
CC treatment of condi- tions or diseases involving PTH. The peptides are
CC pref. prepd. by solid phase synthesis. See also AAR21257 (human generic),
CC AAR21258 (bovine generic) and AAR21259 (porcine generic). (Updated on 25-
CC MAR-2003 to correct PA field.)
XX
SQ Sequence 84 AA;

Query Match 61.1%; Score 99; DB 2; Length 84;
Best Local Similarity 74.2%; Pred. No. 0.00013;
Matches 23; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31

```
                ||||||     |  |:|||||||||||||||
Db          1 AVSEIGFMHNLGKHLSSMERVEWLRKKLQDV 31


RESULT 15
AAW17939
ID   AAW17939 standard; peptide; 34 AA.
XX
AC   AAW17939;
XX
DT   29-JUL-1997  (first entry)
XX
DE   Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.
XX
KW   Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW   bone fracture.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /label= OTHER
FT                   /note= "Cyclohexylalanine (Cha)"
FT   Modified-site   11
FT                   /label= OTHER
FT                   /note= "Cha"
FT   Modified-site   34
FT                   /note= "In amide form"
XX
PN   WO9702834-A1.
XX
PD   30-JAN-1997.
XX
PF   03-JUL-1996;   96WO-US011292.
XX
PR   13-JUL-1995;   95US-0001105P.
PR   06-SEP-1995;   95US-0003305P.
PR   29-MAR-1996;   96US-00626186.
XX
PA   (BIOM-) BIOMEASURE INC.
XX
PI   Dong ZX;
XX
DR   WPI; 1997-118819/11.
XX
PT   New variants of human parathyroid hormone 1-34 peptide - which stimulate
PT   bone growth and are used for treatment of osteoporosis and bone fracture.
XX
PS   Claim 5; Page; 33pp; English.
XX
CC   The present sequence is a specific example of a human parathyroid hormone
CC   (hPTH) analogue from fragment 1-34 in which at least one of the amino
CC   acid residues at positions 7, 11, 23, 24, 27, 28 and 31 is
CC   cyclohexylalanine (Cha). In this example the Leu residue at position 7
CC   and the Leu at position 11 in the wild-type have been substituted by Cha.
CC   The hPTH analogues stimulate bone growth and so are useful in human or
CC   veterinary medicine for treatment of osteoporosis and bone fracture,
CC   optionally in conjunction with anti-resorptive therapy (bisphosphonates
CC   and calcitonin). N.B. The present sequence does not appear in the
CC   specification. It corresponds to the known hPTH 1-34 fragment with the
CC   modifications as stated in the claim
XX
SQ   Sequence 34 AA;

  Query Match             60.5%;  Score 98;  DB 2;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 6.9e-05;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||
Db          1 SVSEIQXMHNXGKHLNSMERVEWLRKKLQDV 31
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Search completed: November 21, 2005, 16:10:12
Job time : 142.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:05:13 ; Search time 23.5 Seconds
(without alignments)
126.924 Million cell updates/sec

Title: US-09-475-158A-5
Perfect score: 162
Sequence: 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	92	56.8	115	1	PTHU	parathyroid hormon
2	91	56.2	115	1	PTBO	parathyroid hormon
3	88	54.3	115	2	JC4202	parathyroid hormon
4	84	51.9	115	1	PTPG	parathyroid hormon
5	77	47.5	115	2	A05091	parathyroid hormon
6	72	44.4	105	2	I51851	parathyroid hormon
7	66	40.7	1336	2	T18288	ABC transport prot
8	64	39.5	212	2	T49559	related to proline
9	64	39.5	440	2	S71795	transcription fact
10	64	39.5	543	2	A41211	early growth respo
11	63.5	39.2	644	2	A53184	myc far upstream e
12	63	38.9	425	2	T03605	probable DNA bindi
13	63	38.9	1090	2	A41696	regulatory protein
14	63	38.9	1428	2	T13926	probable protein p
15	63	38.9	1596	2	A33106	neurogenic locus m
16	63	38.9	1858	2	T18273	1-phosphatidylinos
17	62.5	38.6	644	1	I40712	endo-1,4-beta-xyla
18	62	38.3	252	2	T45737	hypothetical prote
19	62	38.3	486	2	C96699	hypothetical prote
20	61.5	38.0	415	2	D96664	hypothetical prote
21	61.5	38.0	1047	2	G87398	AcrB/AcrD/AcrF fam
22	61.5	38.0	1066	2	G84746	hypothetical prote
23	61	37.7	199	2	T49450	hypothetical prote
24	61	37.7	199	2	S16063	acp-22 protein - y
25	61	37.7	199	2	S32224	acp-22 protein - y
26	61	37.7	201	2	T49792	hypothetical prote
27	61	37.7	209	2	D86399	protein F17L21.18
28	61	37.7	594	2	B86456	protein trihelix D
29	61	37.7	649	2	S58064	hdc protein - frui
30	61	37.7	671	2	A35912	homeotic protein o
31	61	37.7	867	2	S57795	probable deoxyribo
32	60	37.0	239	2	S49193	GCR 101 protein -
33	60	37.0	315	2	T41868	hypothetical prote
34	60	37.0	339	2	T06612	hypothetical prote
35	60	37.0	500	2	T20961	hypothetical prote
36	60	37.0	570	2	T27407	hypothetical prote
37	59.5	36.7	455	2	B86427	hypothetical prote
38	59	36.4	201	2	F84596	glycine-rich prote
39	59	36.4	210	2	A42687	neurotrophin-4 pre
40	59	36.4	240	2	A46179	U2 snRNP auxiliary
41	59	36.4	287	2	A60643	antigen 5401 - Eim
42	59	36.4	396	2	T49109	glycine-rich prote
43	59	36.4	433	1	QQBEV2	UL44 protein - hum
44	59	36.4	443	1	S29334	transcription fact
45	59	36.4	445	1	S31224	transcription fact

ALIGNMENTS

RESULT 1
PTHU
parathyroid hormone precursor [validated] - human
N;Alternate names: proparathyroid hormone
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410; I38
R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
A;Title: Nucleotide sequence of the human parathyroid hormone gene.
A;Reference number: A19339; MUID:83169834; PMID:6220408
A;Accession: A19339
A;Molecule type: DNA
A;Residues: 1-115 <VAS>
A;Cross-references: UNIPROT:P01270; UNIPARC:UPI000013290A; GB:J00301; NID:g190702; PIDN
R;Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.
Biol. Chem. Hoppe-Seyler 375, 821-824, 1994
A;Title: Purification of meprin from human kidney and its role in parathyroid hormone d
A;Reference number: S53790; MUID:95225988; PMID:7710697
A;Accession: S53790
A;Molecule type: protein
A;Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>
A;Cross-references: UNIPARC:UPI00001734E1; UNIPARC:UPI00001734E2; UNIPARC:UPI00001734E3
A;Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occurr
R;Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974
A;Title: Structural analysis of human proparathyroid hormone by a new microsequencing a
A;Reference number: A93169; MUID:74174967; PMID:4833516
A;Accession: A93169
A;Molecule type: protein
A;Residues: 26-37 <JAC>
A;Cross-references: UNIPARC:UPI00001734E4
R;Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.
Eur. J. Biochem. 205, 311-319, 1992
A;Title: Isolation and characterization of two biologically active O-glycosylated forms
ation.
A;Reference number: S21199; MUID:92209518; PMID:1555591
A;Accession: S21199
A;Molecule type: protein
A;Residues: 32-114,'N' <OLS>
A;Cross-references: UNIPARC:UPI00001734E5
A;Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation
R;Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L.H
Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974
A;Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid
A;Reference number: A93789; MUID:74111656; PMID:4521809
A;Accession: A93789
A;Molecule type: protein
A;Residues: 32-68 <NIA>
A;Cross-references: UNIPARC:UPI000002DA05
R;Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A;Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residues 1
A;Reference number: A93783; MUID:73070429; PMID:4509319
A;Accession: A93783
A;Molecule type: protein
A;Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <BRE>
A;Cross-references: UNIPARC:UPI00001734E6
A;Note: this sequence was determined by sequenator and mass spectroscopic identification
R;Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 14, 1842-1847, 1975
A;Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
A;Reference number: A90387; MUID:75146516; PMID:1125201
A;Accession: A90387
A;Molecule type: protein
A;Residues: 52-75 <KE3>
A;Cross-references: UNIPARC:UPI00001734E7
R;Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 17, 5723-5729, 1978
A;Title: Complete amino acid sequence of human parathyroid hormone.
A;Reference number: A90426; MUID:79082855; PMID:728431
A;Accession: A90426
A;Molecule type: protein
A;Residues: 61-106,'D',108-115 <KEU>
A;Cross-references: UNIPARC:UPI00001734E8
R;Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-
A;Reference number: A94410
A;Accession: A94410
A;Molecule type: protein
A;Residues: 75-100 <KE2>
A;Cross-references: UNIPARC:UPI00001734E9
R;Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J
Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
A;Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum
A;Reference number: A91660; MUID:75059220; PMID:4474131
A;Contents: annotation; synthesis of residues 32-65
A;Note: the biologically active amino-terminal 34 residues of parathyroid hormone were s
at renal adenylate cyclase assay and with the bovine hormone's active region in the chic
R;Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel,
Helv. Chim. Acta 56, 470-473, 1973
A;Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
A;Reference number: A91635; MUID:73227467; PMID:4721748
A;Contents: annotation; synthesis of residues 32-65
A;Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined
into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
R;Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
A;Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
A;Reference number: I38342; MUID:82150870; PMID:6950381
A;Accession: I38342
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: UNIPARC:UPI000013290A; EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PID
C;Genetics:
A;Gene: GDB:PTH
A;Cross-references: GDB:119522; OMIM:168450
A;Map position: 11p15.2-11p15.1
A;Introns: 29/2
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: factor in homeostatic control of plasma calcium and phosphate; released b
counter to calcitonin
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland; plasma
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 56.8%; Score 92; DB 1; Length 115;
Best Local Similarity 71.0%; Pred. No. 0.00047;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
:|||| | ||||||||||||||||
Db 32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62

RESULT 2
PTBO
parathyroid hormone precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534
R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.
Gene 28, 319-329, 1984
A;Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroid ho
A;Reference number: A24949; MUID:84262483; PMID:6086460
A;Accession: A24949
A;Molecule type: DNA
A;Residues: 1-115 <WEA>
A;Cross-references: UNIPROT:P01268; UNIPARC:UPI0000132907; GB:K01938
R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr.,
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979
A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid hormo
A;Reference number: A93835; MUID:80056617; PMID:388425
A;Accession: A93835
A;Molecule type: DNA
A;Residues: 1-115 <KRO>
A;Cross-references: UNIPARC:UPI0000132907; GB:V00106; GB:J00023; NID:g84; PIDN:CAA23439 J
A;Note: the authors translated the codon GAA for residue 50 as Gly
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.V
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974
A;Title: The N-terminal amino-acid sequence of bovine proparathyroid hormone.
A;Reference number: A93793; MUID:74142666; PMID:4522780
A;Accession: A93793
A;Molecule type: protein
A;Residues: 26-115 <HAM>
A;Cross-references: UNIPARC:UPI00001734DF
R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; Potts
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970
A;Title: The amino acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162; PMID:5531031
A;Accession: A91648
A;Molecule type: protein
A;Residues: 32-115 <NIA>
A;Cross-references: UNIPARC:UPI00000473E4
R;Brewer Jr., H.B.; Ronan, R.
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970
A;Title: Bovine parathyroid hormone: amino acid sequence.
A;Reference number: A93773; MUID:71063634; PMID:5275384
A;Accession: A93773
A;Molecule type: protein
A;Residues: 32-115 <BRE>
A;Cross-references: UNIPARC:UPI00000473E4
R;Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.;
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
A;Title: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyro
A;Reference number: A93776; MUID:71091588; PMID:4322265
A;Contents: annotation; synthesis of residues 32-65
A;Note: the synthetic peptide was active in vivo and in vitro
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
R;Weaver, C.A.; Gordon, D.F.
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
A;Title: introduction by molecular cloning of artifactual inverted sequences at the 5' te
A;Reference number: I45975; MUID:82037785; PMID:6170060
A;Accession: I45975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE2>
A;Cross-references: UNIPARC:UPI0000132907; GB:J00024; NID:g163642; PIDN:AAA30747.1; PID g
R;Weaver, C.A.; Gordon, D.F.

Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: I45976; MUID:83105964; PMID:6185374
A;Accession: I45976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE3>
A;Cross-references: UNIPARC:UPI0000132907; GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:
C;Genetics:
A;Gene: PTH
A;Introns: 29/2
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-115/Product: proparathyroid hormone #status experimental <PMAT>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 56.2%; Score 91; DB 1; Length 115;
Best Local Similarity 71.0%; Pred. No. 0.00062;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
Db 32 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62

RESULT 3
JC4202
parathyroid hormone precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C;Accession: JC4202
R;Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.C.
Gene 160, 241-243, 1995
A;Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein and
A;Reference number: JC4201; MUID:95369696; PMID:7642102
A;Accession: JC4202
A;Molecule type: mRNA
A;Residues: 1-115 <ROS>
A;Cross-references: UNIPROT:P52212; UNIPARC:UPI0000132908; GB:U15662; NID:g558915; PIDN:
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-31/Domain: signal sequence #status predicted <SIG>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status predicted <MAT>

Query Match 54.3%; Score 88; DB 2; Length 115;
Best Local Similarity 67.7%; Pred. No. 0.0014;
Matches 21; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
Db 32 SVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62

RESULT 4
PTPG
parathyroid hormone precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: B26806; A90390; A90376; A01535
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: B26806
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: UNIPROT:P01269; UNIPARC:UPI000013290B; GB:X05722; GB:Y00409; NID:g18
R;Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Biochemistry 14, 3631-3635, 1975
A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial amino
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Accession: A90390
A;Molecule type: protein
A;Residues: 26-115 <CHU>
A;Cross-references: UNIPARC:UPI00001592DF
R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J
Biochemistry 13, 1994-1999, 1974
A;Title: The amino acid sequence of porcine parathyroid hormone.
A;Reference number: A90376; MUID:74253317; PMID:4840833
A;Accession: A90376
A;Molecule type: protein
A;Residues: 32-109 <SAU>
A;Cross-references: UNIPARC:UPI00001734E0
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormor
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 51.9%; Score 84; DB 1; Length 115;
Best Local Similarity 64.5%; Pred. No. 0.0041;
Matches 20; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
Db 32 SVSEIQLMHNLGKHLSSLERVEWLRKKLQDV 62

RESULT 5
A05091
parathyroid hormone precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05091; A26806
R;Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
J. Biol. Chem. 259, 3320-3329, 1984
A;Reference number: A05091; MUID:84135846; PMID:6321505
A;Accession: A05091
A;Molecule type: DNA
A;Residues: 1-115 <HEI>
A;Cross-references: UNIPROT:P04089; UNIPARC:UPI000013290C; GB:K01268; NID:g206483; PIDN
A;Note: the authors translated the codon GAA for residue 87 as Asp
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hor
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: A26806
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: UNIPARC:UPI000013290C; GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA29
C;Genetics:
A;Introns: 29/3
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;30-64/Domain: parathyroid hormone homology <PTH>

Query Match 47.5%; Score 77; DB 2; Length 115;
Best Local Similarity 61.3%; Pred. No. 0.028;
Matches 19; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
Db 32 AVSEIQLMHNLGKHLASVERMQWLRKKLQDV 62

```
RESULT 6
I51851
parathyroid hormone - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I51851
R;Schmelzer, H.
Adv. Gene Technol. 21, 228-229, 1984
A;Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A;Reference number: I51851
A;Accession: I51851
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-105 <RES>
A;Cross-references: UNIPARC:UPI0000170AE0; GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:
C;Genetics:
A;Gene: PTH
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;20-54/Domain: parathyroid hormone homology <PTH>

  Query Match             44.4%;  Score 72;  DB 2;  Length 105;
  Best Local Similarity   56.7%;  Pred. No. 0.098;
  Matches   17;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQD 30
              |:|||       |  | |:||::||||||||
Db         22 AISEIQLMHNLGKHLASVERMQWLRKKLQD 51


RESULT 7
T18288
ABC transport protein - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18288
R;Loomis, W.F.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z18857
A;Accession: T18288
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1336 <LOO>
A;Cross-references: UNIPROT:Q94479; UNIPARC:UPI000017B173; EMBL:U66526; NID:g1513297; PI
C;Genetics:
A;Gene: abcA

  Query Match             40.7%;  Score 66;  DB 2;  Length 1336;
  Best Local Similarity   70.6%;  Pred. No. 6.1;
  Matches   12;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVE 22
              |||||||||:|: |  |
Db        848 GGGGGGGGGVNNDEENE 864


RESULT 8
T49559
related to proline transport protein [imported] - Neurospora crassa
N;Alternate names: protein B2O8.70
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49559
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49559
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 <SCH>
A;Cross-references: UNIPARC:UPI000017B504; EMBL:AL355930; GSPDB:GN00116; NCSP:B2O8.70
A;Experimental source: BAC clone B2O8; strain OR74A
C;Genetics:
A;Gene: NCSP:B2O8.70
A;Map position: 6

  Query Match             39.5%;  Score 64;  DB 2;  Length 212;
  Best Local Similarity   45.8%;  Pred. No. 1.7;
  Matches   11;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 VSEIGGGGGGGGGLNSMERVEWLR 25
              : :| |||||||| :    | ::|
Db        102 IGQIRGGGGGGGGADGRLHVHYIR 125


RESULT 9
S71795
transcription factor CBF-2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C;Accession: S71795
R;Yuasa, J.; Hirano, S.; Yamagata, M.; Noda, M.
Nature 382, 632-635, 1996
A;Title: Visual projection map specified by topographic expression of transcription factc
A;Reference number: S71794; MUID:96338226; PMID:8757134
A;Accession: S71795
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-440 <YUA>
A;Cross-references: UNIPROT:Q98937; UNIPARC:UPI000012ADD7; EMBL:U47276; NID:g1546783; PII
F;143-234/Domain: fork head DNA-binding domain homology <FHD>

  Query Match             39.5%;  Score 64;  DB 2;  Length 440;
  Best Local Similarity   84.6%;  Pred. No. 3.5;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSM 18
              ||||||||| ||:
Db        129 GGGGGGGGGKNSL 141


RESULT 10
A41211
early growth response protein 1 - human
N;Alternate names: zinc finger protein 225
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A41211; S10504; JX0207
R;Wright, J.J.; Gunter, K.C.; Mitsuya, H.; Irving, S.G.; Kelly, K.; Siebenlist, U.
Science 248, 588-591, 1990
A;Title: Expression of a zinc finger gene in HTLV-I- and HTLV-II-transformed cells.
A;Reference number: A41211; MUID:90239549; PMID:2110381
A;Accession: A41211
A;Molecule type: mRNA
A;Residues: 1-543 <WRI>
A;Cross-references: UNIPROT:P18146; UNIPARC:UPI00000008CD; GB:M80583
R;Suggs, S.V.; Katzowitz, J.L.; Tsai-Morris, C.; Sukhatme, V.P.
Nucleic Acids Res. 18, 4283, 1990
A;Title: cDNA sequence of the human cellular early growth response gene Egr-1.
A;Reference number: S10504; MUID:90332455; PMID:2377485
A;Accession: S10504
A;Molecule type: mRNA
A;Residues: 1-543 <SUG>
A;Cross-references: UNIPARC:UPI00000008CD; EMBL:X52541; NID:g31129; PIDN:CAA36777.1; PID
R;Shimizu, N.; Ohta, M.; Fujiwara, C.; Sagara, J.; Mochizuki, N.; Oda, T.; Utiyama, H.
J. Biochem. 111, 272-277, 1992
A;Title: A gene coding for a zinc finger protein is induced during 12-O-tetradecanoylpho
A;Reference number: JX0207; MUID:92234994; PMID:1569051
A;Accession: JX0207
A;Molecule type: mRNA
A;Residues: 1-543 <SHI>
A;Cross-references: UNIPARC:UPI00000008CD; GB:M62829; NID:g182262; PIDN:AAA35815.1; PID
C;Genetics:
A;Gene: GDB:EGR1
A;Cross-references: GDB:119863; OMIM:128990
A;Map position: 5q31.1-5q31.1
C;Keywords: DNA binding; transcription regulation; zinc finger
```

```
F;340-419/Domain: DNA binding #status predicted <DNB>

  Query Match             39.5%;  Score 64;  DB 2;  Length 543;
  Best Local Similarity   80.0%;  Pred. No. 4.3;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 SEIGGGGGGGGGLNS 17
              |  ||||||||| ||
Db         65 SSSGGGGGGGGGSNS 79


RESULT 11
A53184
myc far upstream element-binding protein - human
N;Alternate names: FUSE-binding protein
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53184
R;Duncan, R.; Bazar, L.; Michelotti, G.; Tomonaga, T.; Krutzsch, H.; Avigan, M.; Levens,
Genes Dev. 8, 465-480, 1994
A;Title: A sequence-specific, single-strand binding protein activates the far upstream e
A;Reference number: A53184; MUID:94170991; PMID:8125259
A;Accession: A53184
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-644 <DUN>
A;Cross-references: UNIPARC:UPI000017C2AF; GB:U05040; NID:g460151; PIDN:AAA17976.1; PID:
C;Keywords: DNA binding

  Query Match             39.2%;  Score 63.5;  DB 2;  Length 644;
  Best Local Similarity   42.9%;  Pred. No. 5.9;
  Matches   12;  Conservative    6;  Mismatches    5;  Indels    5;  Gaps    1;

Qy          6 GGGGGGGGGLN-----SMERVEWLRKKL 28
              |||||||||:|     :::|   :  |:
Db         18 GGGGGGGGGVNDAFKDALQRARQIAAKI 45


RESULT 12
T03605
probable DNA binding protein - rice
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C;Accession: T03605
R;Nakase, M.; Aoki, N.; Matsuda, T.; Adachi, T.
Plant Mol. Biol. 33, 513-522, 1997
A;Title: Characterization of a novel rice bZIP protein which binds to the alpha-globulin
A;Reference number: Z14974; MUID:97201485; PMID:9049271
A;Accession: T03605
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-425 <NAK>
A;Cross-references: UNIPROT:P93405; UNIPARC:UPI00000A1985; EMBL:D78609; NID:g1122224; PI
A;Experimental source: subsp. Japonica, cv. Nipponbare, endosperm
C;Superfamily: BZIP protein; fos/jun DNA-binding domain homology

  Query Match             38.9%;  Score 63;  DB 2;  Length 425;
  Best Local Similarity   53.3%;  Pred. No. 4.5;
  Matches   16;  Conservative    3;  Mismatches    7;  Indels    4;  Gaps    2;

Qy          2 VSEIGGGG--GGGGGLNSMERV--EWLRKK 27
              |:  ||||  ||||| |:| |   ||  :|
Db         35 VASGGGGGVAGGGGGGNAMNRCPSEWYFQK 64


RESULT 13
A41696
regulatory protein nit-4 - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C;Accession: A41696; S37629; S20033
R;Yuan, G.F.; Fu, Y.H.; Marzluf, G.A.
Mol. Cell. Biol. 11, 5735-5745, 1991
A;Title: nit-4, a pathway-specific regulatory gene of Neurospora crassa, encodes a prote
A;Reference number: A41696; MUID:92017855; PMID:1840634
A;Accession: A41696
A;Molecule type: DNA
A;Residues: 1-1090 <YUA>
A;Cross-references: UNIPROT:P28349; UNIPARC:UPI00001301D7; GB:M80368
R;Yuan, G.F.; Fu, Y.H.; Marzluf, G.A.
submitted to the EMBL Data Library, December 1991
A;Description: nit-4, a pathway-specific regulatory gene of Neurospora crassa, encodes a
A;Reference number: S37629
A;Accession: S37629
A;Molecule type: DNA
A;Residues: 1-98,'P',99-466,'S',468-1090 <YU2>
A;Cross-references: UNIPARC:UPI0000168940; EMBL:M80368; NID:g168848; PIDN:AAA33602.1; PI
C;Genetics:
A;Gene: nit-4
A;Introns: 529/2
C;Keywords: DNA binding; nucleus; transcription regulation; zinc finger
F;48-86/Domain: GAL4 zinc binuclear cluster homology <GAL4>

  Query Match             38.9%;  Score 63;  DB 2;  Length 1090;
  Best Local Similarity   48.0%;  Pred. No. 11;
  Matches   12;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          5 IGGGGGGGGGLNSMERVEWLRKKLQ 29
              ||||||||||     : :  |:: |
Db        977 IGGGGGGGGGSTGQRQQQQQRQQQQ 1001


RESULT 14
T13926
probable protein phosphatase 2C1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13926
R;Dick, T.; Bahri, S.M.; Chia, W.
Gene 199, 139-143, 1997
A;Title: Drosophila DPP2C1, a novel member of the protein phosphatase 2C (PP2C) family.
A;Reference number: Z17810; MUID:98019081; PMID:9358049
A;Accession: T13926
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1428 <DIC>
A;Cross-references: UNIPROT:O77023; UNIPARC:UPI000007E714; EMBL:U96697; NID:g3403155; PI
C;Genetics:
A;Gene: dpp2c1
A;Cross-references: FlyBase:FBgn0022768
A;Map position: X

  Query Match             38.9%;  Score 63;  DB 2;  Length 1428;
  Best Local Similarity   64.7%;  Pred. No. 15;
  Matches   11;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGLNS 17
              |   :||||||||| |
Db       1124 AAGRVGGGGGGGGRGS 1140


RESULT 15
A33106
neurogenic locus mam protein - fruit fly (Drosophila melanogaster)
N;Alternate names: mastermind protein
C;Species: Drosophila melanogaster
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: A36391; A33106; S13514
R;Smoller, D.; Friedel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B.
Genes Dev. 4, 1688-1700, 1990
A;Title: The Drosophila neurogenic locus mastermind encodes a nuclear protein unusually
A;Reference number: A36391; MUID:91065516; PMID:1701150
A;Accession: A36391
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1596 <SMO>
```

A;Cross-references: UNIPROT:P21519; UNIPARC:UPI000012EB74; GB:X54251; NID:g8203; PIDN:CA
A;Note: strain Canton S
C;Genetics:
A;Gene: FlyBase:mam
A;Cross-references: FlyBase:FBgn0002643

Query Match 38.9%; Score 63; DB 2; Length 1596;
Best Local Similarity 84.6%; Pred. No. 16;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          5 IGGGGGGGGLNS 17
              :|||||||||| ||
Db        354 VGGGGGGGGGNS 366
```

Search completed: November 21, 2005, 16:17:16
Job time : 24.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 15:55:27 ; Search time 146.5 Seconds
(without alignments)
149.293 Million cell updates/sec

Title: US-09-475-158A-5
Perfect score: 162
Sequence: 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	92	56.8	115	1	PTHY_HUMAN	P01270 homo sapien
2	92	56.8	115	1	PTHY_MACFA	Q9xt35 macaca fasc
3	92	56.8	115	2	Q4VB48_HUMAN	Q4vb48 homo sapien
4	91	56.2	115	1	PTHY_BOVIN	P01268 bos taurus
5	88	54.3	86	2	Q9N1V0_HORSE	Q9n1v0 equus cabal
6	88	54.3	115	1	PTHY_CANFA	P52212 canis famil
7	84	51.9	115	1	PTHY_PIG	P01269 sus scrofa
8	81	50.0	115	1	PTHY_FELCA	Q9gl67 felis silve
9	77	47.5	105	2	Q80WZ2_RAT	Q80wz2 rattus norv
10	77	47.5	115	1	PTHY_RAT	P04089 rattus norv
11	75	46.3	115	2	Q9Z0L6_MOUSE	Q9z016 mus musculu
12	73.5	45.4	1493	1	M3K1_MOUSE	P53349 mus musculu
13	70.5	43.5	770	2	Q6K708_ORYSA	Q6k708 oryza sativ
14	70.5	43.5	836	2	Q6T5K2_ORYSA	Q6t5k2 oryza sativ
15	70.5	43.5	836	2	Q944U1_ORYSA	Q944u1 oryza sativ
16	70	43.2	565	2	Q7S5U3_NEUCR	Q7s5u3 neurospora
17	70	43.2	581	2	Q4IQD8_GIBZE	Q4iqd8 gibberella
18	69.5	42.9	1596	2	Q5KRJ6_CORGL	Q5krj6 corynebacte
19	69	42.6	138	2	Q8LN95_ORYSA	Q8ln95 oryza sativ
20	69	42.6	913	2	Q6PF28_XENLA	Q6pf28 xenopus lae
21	68.5	42.3	420	2	Q94H89_ORYSA	Q94h89 oryza sativ
22	68	42.0	444	2	Q69IL7_ORYSA	Q69il7 oryza sativ
23	68	42.0	454	2	O73627_ANOCA	O73627 anolis caro
24	68	42.0	481	2	Q5N802_ORYSA	Q5n802 oryza sativ
25	68	42.0	555	2	Q7PYH7_ANOGA	Q7pyh7 anopheles g
26	68	42.0	591	2	Q55S19_CRYNE	Q55s19 cryptococcu
27	68	42.0	591	2	Q5KGH1_CRYNE	Q5kgh1 cryptococcu
28	67.5	41.7	325	2	Q6MJT1_BDEBA	Q6mjt1 bdellovibri
29	67.5	41.7	524	2	Q59MN9_CANAL	Q59mn9 candida alb
30	67	41.4	425	2	Q7S5T5_NEUCR	Q7s5t5 neurospora
31	67	41.4	620	2	O62004_BRAFL	O62004 branchiosto
32	67	41.4	634	2	Q54UJ4_DICDI	Q54uj4 dictyosteli
33	67	41.4	836	2	Q8GST0_ORYSA	Q8gst0 oryza sativ
34	67	41.4	959	2	Q561F7_CRYNE	Q561f7 cryptococcu
35	67	41.4	985	2	Q5KQ88_CRYNE	Q5kq88 cryptococcu
36	66.5	41.0	137	2	Q69K54_ORYSA	Q69k54 oryza sativ
37	66.5	41.0	531	2	Q9SQK7_ARATH	Q9sqk7 arabidopsis
38	66.5	41.0	822	2	Q7XCT3_ORYSA	Q7xct3 oryza sativ
39	66.5	41.0	822	2	Q94HZ3_ORYSA	Q94hz3 oryza sativ
40	66	40.7	362	2	Q6Z2M3_ORYSA	Q6z2m3 oryza sativ
41	66	40.7	422	2	O96755_BRALA	O96755 branchiosto
42	66	40.7	559	2	Q54Y02_DICDI	Q54y02 dictyosteli
43	66	40.7	637	2	Q75HJ0_ORYSA	Q75hj0 oryza sativ
44	66	40.7	766	2	Q4SGK9_TETNG	Q4sgk9 tetraodon n
45	66	40.7	1513	2	Q559C0_DICDI	Q559c0 dictyosteli

ALIGNMENTS

RESULT 1
PTHY_HUMAN
ID PTHY_HUMAN STANDARD; PRT; 115 AA.
AC P01270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).
GN Name=PTH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82150870; PubMed=6950381;
RA Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;
RT "Nucleotide sequence of cloned cDNAs encoding human preproparathyroid
RT hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83169834; PubMed=6220408;
RA Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J., Hendy G.N.,
RA Potts J.T. Jr., Rich A., Kronenberg H.M.;
RT "Nucleotide sequence of the human parathyroid hormone gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
RN [3]
RP PROTEIN SEQUENCE OF 26-37.
RX MEDLINE=74174967; PubMed=4833516;
RA Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;
RT "Structural analysis of human proparathyroid hormone by a new
RT microsequencing approach.";
RL Nature 249:155-157(1974).
RN [4]
RP PROTEIN SEQUENCE OF 26-40.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [5]
RP PROTEIN SEQUENCE OF 32-68.
RX MEDLINE=74111656; PubMed=4521809;
RA Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
RA O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;
RT "The amino-acid sequence of the amino-terminal 37 residues of human
RT parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).
RN [6]
RP PROTEIN SEQUENCE OF 61-83 AND 84-115.
RX MEDLINE=79082855; PubMed=728431;
RA Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,

```
RA   Potts J.T. Jr.;
RT   "Complete amino acid sequence of human parathyroid hormone.";
RL   Biochemistry 17:5723-5729(1978).
RN   [7]
RP   PROTEIN SEQUENCE OF 75-100.
RA   Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,
RA   O'Riordan J.L.H., Potts J.T. Jr.;
RL   (In) Talmadge R.V., Owen M., Parsons J.A. (eds.);
RL   Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,
RL   Amsterdam (1975).
RN   [8]
RP   SEQUENCE REVISION.
RX   MEDLINE=75146516; PubMed=1125201;
RA   Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "A reinvestigation of the amino-terminal sequence of human parathyroid
RT   hormone.";
RL   Biochemistry 14:1842-1847(1975).
RN   [9]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=75059220; PubMed=4474131;
RA   Tregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T.,
RA   Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "Solid-phase synthesis of the biologically active N-terminal 1-34
RT   peptide of human parathyroid hormone.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
RN   [10]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=73227467; PubMed=4721748;
RA   Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
RA   Riniker B., Rittel W., Sieber P.;
RT   "Synthesis of sequence 1-34 of human parathyroid hormone.";
RL   Helv. Chim. Acta 56:470-473(1973).
RN   [11]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=91299748; PubMed=2069952;
RA   Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
RT   "Investigation of the solution structure of the human parathyroid
RT   hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and
RT   molecular dynamics calculations.";
RL   Biochemistry 30:6936-6942(1991).
RN   [12]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=93345518; PubMed=8344299;
RA   Barden J.A., Cuthbertson R.M.;
RT   "Stabilized NMR structure of human parathyroid hormone(1-34).";
RL   Eur. J. Biochem. 215:315-321(1993).
RN   [13]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;
RA   Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
RA   Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
RA   Roesch P.;
RT   "Structure of human parathyroid hormone 1-37 in solution.";
RL   J. Biol. Chem. 270:15194-15202(1995).
RN   [14]
RP   STRUCTURE BY NMR OF 32-70.
RX   MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments hPTH(1-34)
RT   and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
RN   [15]
RP   VARIANT FIH ARG-18.
RX   MEDLINE=91009811; PubMed=2212001;
RA   Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
RA   Kronenberg H.M.;
RT   "Mutation of the signal peptide-encoding region of the
RT   preproparathyroid hormone gene in familial isolated
RT   hypoparathyroidism.";
RL   J. Clin. Invest. 86:1084-1087(1990).
RN   [16]
RP   VARIANT FIH PRO-23.
RX   PubMed=10523031;
RA   Sunthornthepvarakul T., Churesigaew S., Ngowngarmratana S.;
RT   "A novel mutation of the signal peptide of the preproparathyroid
RT   hormone gene associated with autosomal recessive familial isolated
RT   hypoparathyroidism.";
RL   J. Clin. Endocrinol. Metab. 84:3792-3796(1999).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- DISEASE: Defects in PTH are a cause of familial isolated
CC       hypoparathyroidism (FIH) [MIM:146200]. FIH exist both as autosomal
CC       dominant and recessive forms of hypoparathyroidism.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; J00301; AAA60215.1; -; Genomic_DNA.
DR   EMBL; V00597; CAA23843.1; -; mRNA.
DR   EMBL; A29146; CAA01956.1; -; Unassigned_DNA.
DR   PIR; A19339; PTHU.
DR   PDB; 1BWX; NMR; @=32-70.
DR   PDB; 1ET1; X-ray; A/B=32-65.
DR   PDB; 1ET2; Model; A=32-65.
DR   PDB; 1FVY; NMR; A=32-62.
DR   PDB; 1HPH; NMR; @=32-68.
DR   PDB; 1HPY; NMR; @=32-65.
DR   PDB; 1HTH; NMR; @=32-65.
DR   PDB; 1ZWA; NMR; @=32-65.
DR   PDB; 1ZWB; NMR; @=33-68.
DR   PDB; 1ZWD; NMR; @=34-68.
DR   PDB; 1ZWE; NMR; @=35-68.
DR   PDB; 1ZWF; NMR; @=35-68.
DR   PDB; 1ZWG; NMR; @=-.
DR   Ensembl; ENSG00000152266; Homo sapiens.
DR   HGNC; HGNC:9606; PTH.
DR   MIM; 168450; -.
DR   MIM; 146200; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   GO; GO:0045453; P:bone resorption; NAS.
DR   GO; GO:0006874; P:calcium ion homeostasis; NAS.
DR   GO; GO:0046058; P:cAMP metabolism; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
DR   GO; GO:0001501; P:skeletal development; TAS.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   3D-structure; Direct protein sequencing; Disease mutation; Hormone;
KW   Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
FT   VARIANT      18     18       C -> R (in FIH; dominant; leads to
FT                                inefficient processing of the precursor).
FT                                /FTId=VAR_006047.
FT   VARIANT      23     23       S -> P (in FIH; recessive, might lead to
FT                                inefficient processing of the precursor).
FT                                /FTId=VAR_018464.
FT   CONFLICT    107    107       N -> D (in Ref. 6).
FT   HELIX        34     64
SQ   SEQUENCE   115 AA;  12861 MW;  849015736A6E5597 CRC64;

  Query Match             56.8%;  Score 92;  DB 1;  Length 115;
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  Best Local Similarity   71.0%;  Pred. No. 0.0031;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||       |  ||||||||||||||||
Db         32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62


RESULT 2
PTHY_MACFA
ID   PTHY_MACFA     STANDARD;      PRT;   115 AA.
AC   Q9XT35;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Malaivijitnond S., Takenaka O.;
RT   "Nucleotide sequences of parathyroid gene in five species of macaque
RT   of Thailand.";
RL   J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AF130257; AAD42777.1; -; Genomic_DNA.
DR   HSSP; P01270; 1ET1.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       By similarity.
FT   PROPEP       26     31       By similarity.
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12890 MW;  8C2500EF24BE5597 CRC64;

  Query Match             56.8%;  Score 92;  DB 1;  Length 115;
  Best Local Similarity   71.0%;  Pred. No. 0.0031;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||       |  ||||||||||||||||
Db         32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62


RESULT 3
Q4VB48_HUMAN
ID   Q4VB48_HUMAN PRELIMINARY;      PRT;   115 AA.
AC   Q4VB48;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Parathyroid hormone, preproprotein.
GN   Name=PTH;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC096143; AAH96143.1; -; mRNA.
DR   EMBL; BC096144; AAH96144.1; -; mRNA.
DR   EMBL; BC096145; AAH96145.1; -; mRNA.
DR   EMBL; BC096142; AAH96142.1; -; mRNA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
SQ   SEQUENCE   115 AA;  12861 MW;  849015736A6E5597 CRC64;

  Query Match             56.8%;  Score 92;  DB 2;  Length 115;
  Best Local Similarity   71.0%;  Pred. No. 0.0031;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||       |  ||||||||||||||||
Db         32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62


RESULT 4
PTHY_BOVIN
ID   PTHY_BOVIN     STANDARD;      PRT;   115 AA.
AC   P01268;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=80056617; PubMed=388425;
```

```
RA   Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA   Potts J.T. Jr., Rich A.;
RT   "Cloning and nucleotide sequence of DNA coding for bovine
RT   preproparathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82037785; PubMed=6170060;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Introduction by molecular cloning of artifactual inverted sequences
RT   at the 5' terminus of the sense strand of bovine parathyroid hormone
RT   cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL   Mol. Cell. Endocrinol. 28:411-424(1982).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84262483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
RA   Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT   "Isolation and complete nucleotide sequence of the gene for bovine
RT   parathyroid hormone.";
RL   Gene 28:319-329(1984).
RN   [5]
RP   PROTEIN SEQUENCE OF 26-115.
RX   MEDLINE=74142666; PubMed=4522780;
RA   Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA   Cohn D.V.;
RT   "The N-terminal amino-acid sequence of bovine proparathyroid
RT   hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN   [6]
RP   PROTEIN SEQUENCE OF 32-115.
RX   MEDLINE=71076162; PubMed=5531031;
RA   Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
RA   Aurbach G.D., Potts J.T. Jr.;
RT   "The amino acid sequence of bovine parathyroid hormone I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN   [7]
RP   PROTEIN SEQUENCE OF 32-115.
RX   MEDLINE=71063634; PubMed=5275384;
RA   Brewer H.B. Jr., Ronan R.;
RT   "Bovine parathyroid hormone: amino acid sequence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN   [8]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=71091588; PubMed=4322265;
RA   Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA   Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT   "Synthesis of a biologically active N-terminal tetratriacontapeptide
RT   of parathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN   [9]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments hPTH(1-34)
RT   and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; V00106; CAA23439.1; -; mRNA.
DR   EMBL; J00024; AAA30747.1; -; mRNA.
DR   EMBL; K01938; AAA30749.1; -; Genomic_DNA.
DR   EMBL; M25082; AAA30748.1; -; mRNA.
DR   PIR; A24949; PTBO.
DR   PDB; 1ZWC; NMR; @=32-68.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   3D-structure; Direct protein sequencing; Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
FT   CONFLICT    106    106       V -> G (in Ref. 4).
FT   HELIX        37     40
FT   TURN         41     42
FT   TURN         51     52
FT   HELIX        53     60
FT   TURN         61     63
SQ   SEQUENCE   115 AA;  12980 MW;  2ED246B348880710 CRC64;

  Query Match             56.2%;  Score 91;  DB 1;  Length 115;
  Best Local Similarity   71.0%;  Pred. No. 0.0041;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||      |  |:|||||||||||||||
Db         32 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62


RESULT 5
Q9N1V0_HORSE
ID   Q9N1V0_HORSE PRELIMINARY;      PRT;    86 AA.
AC   Q9N1V0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Parathyroid hormone (Fragment).
GN   Name=PTH;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;
RA   Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Bowling A.T., Murray J.D.;
RT   "A comparative gene map of the horse (Equus caballus).";
RL   Genome Res. 9:1239-1249(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Shiue Y.-L., Caetano A.R., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Murray J.D., Bowling A.T.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF134233; AAF62347.1; -; Genomic_DNA.
DR   HSSP; P01270; 1ET1.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   86 AA;  9805 MW;  253184EA681A2022 CRC64;
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  Query Match             54.3%;  Score 88;  DB 2;  Length 86;
  Best Local Similarity   67.7%;  Pred. No. 0.0069;
  Matches   21;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  |||:|||||||||||||||
Db          3 SVSEIQLMHNLGKHLNSVERVEWLRKKLQDV 33


RESULT 6
PTHY_CANFA
ID   PTHY_CANFA     STANDARD;      PRT;   115 AA.
AC   P52212;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Parathyroid;
RX   MEDLINE=95369696; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;
RA   Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W.,
RA   Capen C.C.;
RT   "Sequences of the cDNAs encoding canine parathyroid hormone-related
RT   protein and parathyroid hormone.";
RL   Gene 160:241-243(1995).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ----------------------------------------------------------------------
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; U15662; AAA82584.1; -; mRNA.
DR   PIR; JC4202; JC4202.
DR   HSSP; P01268; 1ZWC.
DR   Ensembl; ENSCAFG00000008177; Canis familiaris.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       By similarity.
FT   PROPEP       26     31       By similarity.
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12957 MW;  FC38F77F1C8CFE56 CRC64;

  Query Match             54.3%;  Score 88;  DB 1;  Length 115;
  Best Local Similarity   67.7%;  Pred. No. 0.0093;
  Matches   21;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  |:|||||||||||||||
Db         32 SVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62


RESULT 7
PTHY_PIG
ID   PTHY_PIG       STANDARD;      PRT;   115 AA.
AC   P01269;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [2]
RP   PROTEIN SEQUENCE OF 26-115.
RX   MEDLINE=76018954; PubMed=1164500;
RA   Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
RT   "Porcine proparathyroid hormone. Identification, biosynthesis, and
RT   partial amino acid sequence.";
RL   Biochemistry 14:3631-3635(1975).
RN   [3]
RP   PROTEIN SEQUENCE OF 32-115.
RX   MEDLINE=74253317; PubMed=4840833;
RA   Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA   Potts J.T. Jr.;
RT   "The amino acid sequence of porcine parathyroid hormone.";
RL   Biochemistry 13:1994-1999(1974).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X05722; CAA29193.1; -; mRNA.
DR   PIR; B26806; PTPG.
DR   HSSP; P01270; 1BWX.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Direct protein sequencing; Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12852 MW;  9FE8BCDE614BAC16 CRC64;

  Query Match             51.9%;  Score 84;  DB 1;  Length 115;
  Best Local Similarity   64.5%;  Pred. No. 0.028;
  Matches   20;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  |:|:|||||||||||||
Db         32 SVSEIQLMHNLGKHLSSLERVEWLRKKLQDV 62


RESULT 8
PTHY_FELCA
ID   PTHY_FELCA     STANDARD;      PRT;   115 AA.
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```
AC   Q9GL67;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT   "Molecular cloning of feline preproparathyroid hormone.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF309967; AAG30545.1; -; mRNA.
DR   HSSP; P01268; 1ZWC.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       By similarity.
FT   PROPEP       26     31       By similarity.
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12921 MW;  80CD557CC6A1A47E CRC64;

  Query Match             50.0%;  Score 81;  DB 1;  Length 115;
  Best Local Similarity   61.3%;  Pred. No. 0.063;
  Matches   19;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||       |  |:|:|||||||:|||||
Db         32 SVSEIQFMHNLGKHLSSVERVEWLRRKLQDV 62


RESULT 9
Q80WZ2_RAT
ID   Q80WZ2_RAT  PRELIMINARY;      PRT;   105 AA.
AC   Q80WZ2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothalamic parathyroid hormone.
GN   Name=PTH-(1-84);
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA   Nutley M.T., Parimi S.A., Harvey S.;
RT   "Sequence analysis of hypothalamic parathyroid hormone messenger
RT   ribonucleic acid.";
RL   Endocrinology 136:5600-5607(1995).
DR   EMBL; S80127; AAP32220.1; -; mRNA.
DR   HSSP; P01270; 1ZWB.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
SQ   SEQUENCE   105 AA;  11684 MW;  18EE71B3F1CF5F70 CRC64;

  Query Match             47.5%;  Score 77;  DB 2;  Length 105;
  Best Local Similarity   61.3%;  Pred. No. 0.17;
  Matches   19;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||       |  | |:||::|||||||||
Db         22 AVSEIQLMHNLGKHLASVERMQWLRKKLQDV 52


RESULT 10
PTHY_RAT
ID   PTHY_RAT       STANDARD;      PRT;   115 AA.
AC   P04089; Q63473;
DT   01-NOV-1986 (Rel. 03, Created)
DT   01-NOV-1986 (Rel. 03, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=Pth;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84135846; PubMed=6321505;
RA   Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT   "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
RT   gene and deduced amino acid sequence of rat preproparathyroid
RT   hormone.";
RL   J. Biol. Chem. 259:3320-3329(1984).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 10-115.
RC   TISSUE=Parathyroid;
RA   Schmelzer H.J., Gross G., Mayer H.;
RT   "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
RT   hormone.";
RL   Adv. Gene Technol. 21:228-229(1984).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 32-115.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
RX   MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA   Nutley M.T., Parimi S.A., Harvey S.;
RT   "Sequence analysis of hypothalamic parathyroid hormone messenger
RT   ribonucleic acid.";
RL   Endocrinology 136:5600-5607(1995).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Hypothalamus and parathyroid gland.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
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CC   ----------------------------------------------------------------------
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; K01268; AAA41979.1; -; Genomic_DNA.
DR   EMBL; X05721; CAA29192.1; -; mRNA.
DR   EMBL; M54875; AAA57156.1; -; mRNA.
DR   EMBL; S80127; -; NOT_ANNOTATED_CDS; mRNA.
DR   PIR; A05091; A05091.
DR   HSSP; P01270; 1ZWB.
DR   Ensembl; ENSRNOG00000014318; Rattus norvegicus.
DR   RGD; 3440; Pth.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003626; PTH_related.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD013225; PTH_related; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
FT   CONFLICT     18     18       C -> Y (in Ref. 3).
FT   CONFLICT     23     23       A -> T (in Ref. 3).
FT   CONFLICT     33     33       V -> I (in Ref. 3).
FT   CONFLICT     62     62       V -> G (in Ref. 3).
SQ   SEQUENCE   115 AA;  12722 MW;  7B434CFCA528B230 CRC64;

  Query Match             47.5%;  Score 77;  DB 1;  Length 115;
  Best Local Similarity   61.3%;  Pred. No. 0.19;
  Matches   19;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||       |  | |:||::|||||||||
Db         32 AVSEIQLMHNLGKHLASVERMQWLRKKLQDV 62


RESULT 11
Q9Z0L6_MOUSE
ID   Q9Z0L6_MOUSE PRELIMINARY;      PRT;   115 AA.
AC   Q9Z0L6;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Parathyroid hormone precursor.
GN   Name=Pth;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/Sv;
RA   Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.;
RT   "Cloning of the murine gene encoding parathyroid hormone: genomic
RT   organization and nucleotide sequence.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thyroid;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF066075; AAC99656.1; -; Genomic_DNA.
DR   EMBL; BC099456; AAH99456.1; -; mRNA.
DR   HSSP; P01270; 1ZWB.
DR   Ensembl; ENSMUSG00000059077; Mus musculus.
DR   MGI; MGI:97799; Pth.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005179; F:hormone activity; IDA.
DR   GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Signal.
FT   SIGNAL        1     25       Potential.
FT   CHAIN        32    115       parathyroid hormone.
SQ   SEQUENCE   115 AA;  12825 MW;  DA43FABBCB4E2FD9 CRC64;

  Query Match             46.3%;  Score 75;  DB 2;  Length 115;
  Best Local Similarity   58.1%;  Pred. No. 0.33;
  Matches   18;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||       |  | ||||::|||:||||:
Db         32 AVSEIQLMHNLGKHLASMERMQWLRRKLQDM 62


RESULT 12
M3K1_MOUSE
ID   M3K1_MOUSE     STANDARD;      PRT;  1493 AA.
AC   P53349; Q60831; Q9R0U3; Q9R256;
DT   01-OCT-1996 (Rel. 34, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.37)
DE   (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1).
GN   Name=Map3k1; Synonyms=Mekk, Mekk1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lange C.A., Blumer K.J., Sather S.L., Johnson G.L.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 1-659.
RC   TISSUE=Spleen;
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RX   MEDLINE=99455010; PubMed=10523642;
RA   Ito M., Yoshioka K., Akechi M., Yamashita S., Takamatsu N.,
RA   Sugiyama K., Hibi M., Nakabeppu Y., Shiba T., Yamamoto K.-I.;
RT   "JSAP1, a novel jun N-terminal protein kinase (JNK)-binding protein
RT   that functions as a scaffold factor in the JNK signaling pathway.";
RL   Mol. Cell. Biol. 19:7539-7548(1999).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 660-1493.
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=93227040; PubMed=8385802;
RA   Lange-Carter C.A., Pleiman C.M., Gardner A.M., Blumer K.J.,
RA   Johnson G.L.;
RT   "A divergence in the MAP kinase regulatory network defined by MEK
RT   kinase and Raf.";
RL   Science 260:315-319(1993).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 796-1493.
RC   STRAIN=BALB/c; TISSUE=Heart;
RA   Whitmarsh A.J., Shore P., Sharrocks A.D., Davis R.J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   ENZYME REGULATION, AND MUTAGENESIS OF THR-1381 AND THR-1393.
RX   PubMed=9078260;
RA   Deak J.C., Templeton D.J.;
RT   "Regulation of the activity of MEK kinase 1 (MEKK1) by
RT   autophosphorylation within the kinase activation domain.";
RL   Biochem. J. 322:185-192(1997).
RN   [6]
RP   FUNCTION, INTERACTIONS WITH IKBKB AND MAP2K4, ENZYME REGULATION, AND
RP   MUTAGENESIS OF THR-1381; THR-1393; ISO-1394; PHE-1396; MET-1397;
RP   VAL-1401; LEU-1402; ARG-1403 AND GLY-1404.
RX   PubMed=14500727; DOI=10.1074/jbc.M304234200;
RA   Tu Z., Lee F.S.;
RT   "Subdomain VIII is a specificity-determining region in MEKK1.";
RL   J. Biol. Chem. 278:48498-48505(2003).
CC   -!- FUNCTION: Component of a protein kinase signal transduction
CC       cascade. Activates the ERK and JNK kinase pathways by
CC       phosphorylation of MAP2K1 and MAP2K4. Activates CHUK and IKBKB,
CC       the central protein kinases of the NF-kappa-B pathway.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- COFACTOR: Magnesium.
CC   -!- ENZYME REGULATION: Activated by phosphorylation on Thr-1381 and
CC       Thr-1393.
CC   -!- SUBUNIT: Binds both upstream activators and downstream substrates
CC       in multimolecular complexes through its N-terminus.
CC   -!- INTERACTION:
CC       O88351:Ikbkb; NbExp=1; IntAct=EBI-447913, EBI-447960;
CC       P47809:Map2k4; NbExp=1; IntAct=EBI-447913, EBI-447934;
CC       Q9QZH6:Sitpec; NbExp=1; IntAct=EBI-447913, EBI-527020;
CC   -!- TISSUE SPECIFICITY: Highly expressed in the heart and spleen while
CC       a lower level expression is seen in the liver.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP
CC       kinase kinase kinase subfamily.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- SIMILARITY: Contains 1 SWIM-type zinc finger.
CC   ---------------------------------------------------------------------
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CC   use as long as its content is in no way modified and this statement is not
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CC   ---------------------------------------------------------------------
DR   EMBL; AF117340; AAD25049.1; -; mRNA.
DR   EMBL; AB014614; BAA85878.1; -; mRNA.
DR   EMBL; L13103; AAA97500.1; ALT_INIT; mRNA.
DR   EMBL; U23470; AAA85038.1; -; mRNA.
DR   HSSP; Q16539; 1KV1.
DR   IntAct; P53349; -.
DR   Ensembl; ENSMUSG00000021754; Mus musculus.
DR   MGI; MGI:1346872; Map3k1.
DR   GO; GO:0001747; P:eye morphogenesis (sensu Mammalia); IMP.
DR   GO; GO:0030838; P:positive regulation of actin filament polym. . .; IMP.
DR   GO; GO:0030334; P:regulation of cell migration; IMP.
DR   GO; GO:0007179; P:transforming growth factor beta receptor si. . .; IMP.
DR   GO; GO:0042060; P:wound healing; IMP.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR003903; UIM.
DR   InterPro; IPR001841; Znf_RING.
DR   InterPro; IPR007527; Znf_SWIM.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF04434; SWIM; 1.
DR   Pfam; PF02809; UIM; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
DR   PROSITE; PS50966; ZF_SWIM; 1.
KW   ATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide-binding;
KW   Phosphorylation; Serine/threonine-protein kinase; Transferase; Zinc;
KW   Zinc-finger.
FT   DOMAIN     1224   1489       Protein kinase.
FT   ZN_FING     333    361       SWIM-type.
FT   ZN_FING     438    487       RING-type.
FT   NP_BIND    1230   1238       ATP (By similarity).
FT   COMPBIAS     25     32       Poly-Gly.
FT   COMPBIAS     74    149       Pro-rich.
FT   COMPBIAS    233    291       Pro-rich.
FT   COMPBIAS    417    426       Poly-Ser.
FT   ACT_SITE   1350   1350       Proton acceptor (By similarity).
FT   BINDING    1253   1253       ATP (By similarity).
FT   MOD_RES    1381   1381       Phosphothreonine.
FT   MOD_RES    1393   1393       Phosphothreonine.
FT   MUTAGEN    1381   1381       T->A: Fails to activate MAP2K1, MAP2K4,
FT                                MAP2K7, CHUK and IKBKB.
FT   MUTAGEN    1381   1381       T->E: Loss of kinase activity and
FT                                autophosphorylation.
FT   MUTAGEN    1381   1381       T->S: Reduced kinase activity and
FT                                autophosphorylation.
FT   MUTAGEN    1393   1393       T->A: Loss of kinase activity and
FT                                autophosphorylation. Fails to activate
FT                                MAP2K1, MAP2K4, MAP2K7, CHUK and IKBKB.
FT   MUTAGEN    1393   1393       T->E: Loss of kinase activity and
FT                                autophosphorylation.
FT   MUTAGEN    1393   1393       T->S: Reduced kinase activity and
FT                                autophosphorylation.
FT   MUTAGEN    1394   1394       I->A: Loss of NF-kappa-B transcription
FT                                factor activity and reduced ability to
FT                                activate MAP2K1, MAP2K4, MAP2K7. No
FT                                effect on AP-1 activity or activation of
FT                                CHUK and IKBKB. Loss of binding to IKBKB.
FT   MUTAGEN    1396   1396       F->A: Loss of AP-1 and NF-kappa-B
FT                                transcription factor activity. Reduced
FT                                ability to activate MAP2K1, MAP2K4,
FT                                MAP2K7, CHUK and IKBKB.
FT   MUTAGEN    1397   1397       M->A: Loss of AP-1 and NF-kappa-B
FT                                transcription factor activity. Reduced
FT                                ability to activate MAP2K1, MAP2K4,
FT                                MAP2K7, CHUK and IKBKB.
FT   MUTAGEN    1401   1401       V->A: Loss of AP-1 and NF-kappa-B
FT                                transcription factor activity. Reduced
FT                                ability to activate MAP2K1, MAP2K4,
FT                                MAP2K7, CHUK and IKBKB.
FT   MUTAGEN    1402   1402       L->A: Loss of AP-1 transcription factor
FT                                activity and reduced ability to activate
FT                                CHUK and IKBKB. No effect on NF-kappa-B
FT                                activity or activation of MAP2K1, MAP2K4,
FT                                MAP2K7. Loss of binding to MAP2K4.
FT   MUTAGEN    1403   1403       R->A: Loss of AP-1 transcription factor
FT                                activity, no effect on NF-kappa-B
```

```
FT                                activity.
FT   MUTAGEN    1404   1404       G->A: Loss of AP-1 and NF-kappa-B
FT                                transcription factor activity.
FT   CONFLICT     30     39       GGGALQGSGA -> ALQGSG (in Ref. 2).
FT   CONFLICT    103    103       Missing (in Ref. 2).
FT   CONFLICT    257    257       V -> E (in Ref. 2).
FT   CONFLICT    307    307       M -> V (in Ref. 2).
FT   CONFLICT    413    413       S -> C (in Ref. 2).
FT   CONFLICT    559    559       V -> A (in Ref. 2).
FT   CONFLICT    883    883       V -> L (in Ref. 3).
FT   CONFLICT   1467   1467       V -> L (in Ref. 3).
SQ   SEQUENCE   1493 AA;  161289 MW;  CA65C9B7703C6BF9 CRC64;

  Query Match             45.4%;  Score 73.5;  DB 1;  Length 1493;
  Best Local Similarity   34.0%;  Pred. No. 6.8;
  Matches   17;  Conservative    4;  Mismatches   10;  Indels   19;  Gaps    1;

Qy          1 AVSEIGGGGGGGGGLN------------------SMERVEWLRKKLQDV 31
              |  | |||||||| |                    || :| |::|: |
Db         20 ASPEAGGGGGGGGALQGSGAPAAGAAGLLREPGSAGRERADWRRRQLRKV 69


RESULT 13
Q6K708_ORYSA
ID   Q6K708_ORYSA PRELIMINARY;      PRT;   770 AA.
AC   Q6K708;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Putative ethylene receptor-like protein 2.
GN   Name=P0474F11.19-1; Synonyms=OJ1119_A01.4-1;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
RT   clone:OJ1119_A01.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP004878; BAD23111.1; -; Genomic_DNA.
DR   EMBL; AP004020; BAD22879.1; -; Genomic_DNA.
DR   Gramene; Q6K708; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR005467; His_kinase.
DR   InterPro; IPR003661; His_kinA_N.
DR   InterPro; IPR001789; Response_reg.
DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; HisKA; 1.
DR   Pfam; PF00072; Response_reg; 1.
DR   ProDom; PD000039; Response_reg; 1.
DR   SMART; SM00065; GAF; 1.
DR   SMART; SM00388; HisKA; 1.
DR   SMART; SM00448; REC; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW   Receptor.
SQ   SEQUENCE   770 AA;  84998 MW;  E4F7151DB57B973B CRC64;

  Query Match             43.5%;  Score 70.5;  DB 2;  Length 770;
  Best Local Similarity   55.6%;  Pred. No. 7.8;
  Matches   15;  Conservative    5;  Mismatches    4;  Indels    3;  Gaps    2;

Qy          6 GGGGGGGGGLNSMERV-EWLRKKLQDV 31
              |||||||||| ||: :  |  :|: |:
Db         46 GGGGGGGGGLWSMDSIFRW--QKVSDL 70


RESULT 14
Q6T5K2_ORYSA
ID   Q6T5K2_ORYSA PRELIMINARY;      PRT;   836 AA.
AC   Q6T5K2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative ethylene receptor.
GN   Name=ETR3;
OS   Oryza sativa (indica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39946;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14754915; DOI=10.1093/jxb/erh055;
RA   Yau C.P., Wang L., Yu M., Zee S.Y., Yip W.K.;
RT   "Differential expression of three genes encoding an ethylene receptor
RT   in rice during development, and in response to indole-3-acetic acid
RT   and silver ions.";
RL   J. Exp. Bot. 55:547-556(2004).
DR   EMBL; AY434735; AAR08915.1; -; mRNA.
DR   Gramene; Q6T5K2; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR005467; His_kinase.
DR   InterPro; IPR003661; His_kinA_N.
DR   InterPro; IPR001789; Response_reg.
DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; HisKA; 1.
DR   Pfam; PF00072; Response_reg; 1.
DR   ProDom; PD000039; Response_reg; 1.
DR   SMART; SM00065; GAF; 1.
DR   SMART; SM00388; HisKA; 1.
DR   SMART; SM00448; REC; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW   Receptor.
SQ   SEQUENCE   836 AA;  92644 MW;  324D3E7F0B97A85A CRC64;

  Query Match             43.5%;  Score 70.5;  DB 2;  Length 836;
  Best Local Similarity   55.6%;  Pred. No. 8.5;
  Matches   15;  Conservative    5;  Mismatches    4;  Indels    3;  Gaps    2;

Qy          6 GGGGGGGGGLNSMERV-EWLRKKLQDV 31
              |||||||||| ||: :  |  :|: |:
Db        112 GGGGGGGGGLWSMDSIFRW--QKVSDL 136


RESULT 15
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Q944U1_ORYSA
ID   Q944U1_ORYSA PRELIMINARY;      PRT;   836 AA.
AC   Q944U1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ethylene receptor-like protein 2.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Cao W.H., Dong Y., Zhang J.S., Chen S.Y.;
RT   "Characterization of an ethylene receptor homolog gene from rice.";
RL   Sci. China, Ser. C, Life Sci. 46:370-378(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Zhang J.-S., Dong Y., Chen S.-Y.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF420318; AAL29303.2; -; mRNA.
DR   Gramene; Q944U1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR005467; His_kinase.
DR   InterPro; IPR003661; His_kinA_N.
DR   InterPro; IPR001789; Response_reg.
DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; HisKA; 1.
DR   Pfam; PF00072; Response_reg; 1.
DR   ProDom; PD000039; Response_reg; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW   Receptor.
SQ   SEQUENCE   836 AA;  92644 MW;  324D3E7F0B97A85A CRC64;

  Query Match             43.5%;  Score 70.5;  DB 2;  Length 836;
  Best Local Similarity   55.6%;  Pred. No. 8.5;
  Matches   15;  Conservative    5;  Mismatches    4;  Indels    3;  Gaps    2;

Qy          6 GGGGGGGGGLNSMERV-EWLRKKLQDV 31
              |||||||||| ||: :  |  :|: |:
Db        112 GGGGGGGGGLWSMDSIFRW--QKVSDL 136


Search completed: November 21, 2005, 16:15:13
Job time : 148.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:05:03 ; Search time 33 Seconds
(without alignments)
77.665 Million cell updates/sec

Title: US-09-475-158A-5
Perfect score: 162
Sequence: 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	100	61.7	38	4	PCT-US95-15800-29	Sequence 29, Appl
2	98	60.5	35	1	US-08-142-551B-34	Sequence 34, Appl
3	98	60.5	35	1	US-08-142-551B-37	Sequence 37, Appl
4	98	60.5	35	1	US-08-142-551B-46	Sequence 46, Appl
5	96	59.3	35	1	US-08-142-551B-40	Sequence 40, Appl
6	96	59.3	35	1	US-08-142-551B-52	Sequence 52, Appl
7	96	59.3	35	1	US-08-142-551B-56	Sequence 56, Appl
8	95	58.6	33	2	US-09-447-800-6	Sequence 6, Appli
9	95	58.6	34	2	US-09-447-800-5	Sequence 5, Appli
10	94	58.0	34	2	US-09-044-536A-12	Sequence 12, Appl
11	94	58.0	34	2	US-09-843-221A-17	Sequence 17, Appl
12	94	58.0	34	2	US-09-843-221A-18	Sequence 18, Appl
13	94	58.0	34	2	US-09-843-221A-162	Sequence 162, App
14	94	58.0	34	2	US-09-843-221A-163	Sequence 163, App
15	94	58.0	35	1	US-08-142-551B-43	Sequence 43, Appl
16	93	57.4	34	2	US-09-044-536A-8	Sequence 8, Appli
17	92	56.8	31	1	US-08-262-495C-3	Sequence 3, Appli
18	92	56.8	31	1	US-08-691-647C-1	Sequence 1, Appli
19	92	56.8	31	1	US-08-691-647C-6	Sequence 6, Appli
20	92	56.8	31	2	US-08-904-760B-1	Sequence 1, Appli
21	92	56.8	31	2	US-08-904-760B-6	Sequence 6, Appli
22	92	56.8	31	2	US-08-904-760B-14	Sequence 14, Appl
23	92	56.8	31	2	US-08-904-760B-32	Sequence 32, Appl
24	92	56.8	31	2	US-09-406-813-2	Sequence 2, Appli
25	92	56.8	31	2	US-09-536-785A-1	Sequence 1, Appli
26	92	56.8	31	2	US-09-536-785A-6	Sequence 6, Appli
27	92	56.8	31	2	US-09-536-785A-14	Sequence 14, Appl
28	92	56.8	31	2	US-09-536-785A-32	Sequence 32, Appl
29	92	56.8	31	2	US-09-843-221A-27	Sequence 27, Appl
30	92	56.8	31	2	US-09-843-221A-165	Sequence 165, App
31	92	56.8	31	2	US-09-623-548A-271	Sequence 271, App
32	92	56.8	31	2	US-09-657-276-271	Sequence 271, App
33	92	56.8	33	2	US-09-447-800-9	Sequence 9, Appli
34	92	56.8	34	1	US-07-765-373-1	Sequence 1, Appli
35	92	56.8	34	1	US-08-033-099-1	Sequence 1, Appli
36	92	56.8	34	1	US-08-262-495C-1	Sequence 1, Appli
37	92	56.8	34	1	US-07-915-247A-1	Sequence 1, Appli
38	92	56.8	34	1	US-08-443-863-1	Sequence 1, Appli
39	92	56.8	34	1	US-08-448-070-1	Sequence 1, Appli
40	92	56.8	34	1	US-08-488-105-7	Sequence 7, Appli
41	92	56.8	34	1	US-08-468-275-6	Sequence 6, Appli
42	92	56.8	34	1	US-08-449-500-1	Sequence 1, Appli
43	92	56.8	34	1	US-08-449-317A-1	Sequence 1, Appli
44	92	56.8	34	1	US-08-142-551B-2	Sequence 2, Appli
45	92	56.8	34	1	US-08-477-022-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
PCT-US95-15800-29
; Sequence 29, Application PC/TUS9515800
;  GENERAL INFORMATION:
;    APPLICANT:  BioNebraska, Inc.
;    TITLE OF INVENTION:  PRODUCTION OF PEPTIDES USING
;    TITLE OF INVENTION:  RECOMBINANT FUSION PROTEIN CONSTRICTS
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  3100 Norwest Center, 90 S. 7th Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  U.S.A.
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/15800
;      FILING DATE:  07-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,530
;      FILING DATE:  07-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carter, Charles G
;      REGISTRATION NUMBER:  35,093
;      REFERENCE/DOCKET NUMBER:  8648.45USWO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/332-5300
;      TELEFAX:  612/332-9081
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
PCT-US95-15800-29

  Query Match             61.7%;  Score 100;  DB 4;  Length 38;
  Best Local Similarity   74.2%;  Pred. No. 1.8e-05;
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  Matches   23;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
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Db          1 SVSEIGLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 2
US-08-142-551B-34
; Sequence 34, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-34

  Query Match             60.5%;  Score 98;  DB 1;  Length 35;
  Best Local Similarity   71.0%;  Pred. No. 2.8e-05;
  Matches   22;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :|||| |    |  |||:|||||||||||||
Db          1 SVSEIQGLHNLGKHLNSLERVEWLRKKLQDV 31


RESULT 3
US-08-142-551B-37
; Sequence 37, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-37

  Query Match             60.5%;  Score 98;  DB 1;  Length 35;
  Best Local Similarity   71.0%;  Pred. No. 2.8e-05;
  Matches   22;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :|||| |    |  |||:|||||||||||||
Db          1 SVSEIQLGHNLGKHLNSLERVEWLRKKLQDV 31


RESULT 4
US-08-142-551B-46
; Sequence 46, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
```

```
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-46

  Query Match             60.5%;  Score 98;  DB 1;  Length 35;
  Best Local Similarity   71.0%;  Pred. No. 2.8e-05;
  Matches   22;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||     ||  |||:|||||||||||||
Db          1 SVSEIQLLHNGGKHLNSLERVEWLRKKLQDV 31


RESULT 5
US-08-142-551B-40
; Sequence 40, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-40

  Query Match             59.3%;  Score 96;  DB 1;  Length 35;
  Best Local Similarity   71.0%;  Pred. No. 4.9e-05;
  Matches   22;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||     |  |  |||:|||||||||||||
Db          1 SVSEIQLLGNLGKHLNSLERVEWLRKKLQDV 31


RESULT 6
US-08-142-551B-52
; Sequence 52, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-52

  Query Match             59.3%;  Score 96;  DB 1;  Length 35;
  Best Local Similarity   71.0%;  Pred. No. 4.9e-05;
  Matches   22;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      || |||:|||||||||||||
Db          1 SVSEIQLLHNLGGHLNSLERVEWLRKKLQDV 31


RESULT 7
US-08-142-551B-56
; Sequence 56, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-56

  Query Match             59.3%;  Score 96;  DB 1;  Length 35;
  Best Local Similarity   71.0%;  Pred. No. 4.9e-05;
  Matches   22;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      | ||||:|||||||||||||
Db          1 SVSEIQLLHNLGKGLNSLERVEWLRKKLQDV 31


RESULT 8
US-09-447-800-6
; Sequence 6, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION: ANALOGS
;  FILE REFERENCE: 0609.4630001
;  CURRENT APPLICATION NUMBER: US/09/447,800
;  CURRENT FILING DATE: 1999-11-23
;  EARLIER APPLICATION NUMBER: 60/110,152
;  EARLIER FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-09-447-800-6

  Query Match             58.6%;  Score 95;  DB 2;  Length 33;
  Best Local Similarity   74.2%;  Pred. No. 6.1e-05;
  Matches   23;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||      |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
```

```
RESULT 9
US-09-447-800-5
; Sequence 5, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION: ANALOGS
;  FILE REFERENCE: 0609.4630001
;  CURRENT APPLICATION NUMBER: US/09/447,800
;  CURRENT FILING DATE: 1999-11-23
;  EARLIER APPLICATION NUMBER: 60/110,152
;  EARLIER FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-09-447-800-5

  Query Match             58.6%;  Score 95;  DB 2;  Length 34;
  Best Local Similarity   74.2%;  Pred. No. 6.3e-05;
  Matches   23;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||       |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 10
US-09-044-536A-12
; Sequence 12, Application US/09044536A
; Patent No. 6025467
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  NAKAGAWA, Shizue
;    APPLICANT:  HABASHITA, Junko
;    APPLICANT:  TAKETOMI, Shigehisa
;    TITLE OF INVENTION:  PARATHYROID HORMONE DERIVATIVES AND THEIR USE
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/044,536A
;      FILING DATE:  19-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/662,871
;      FILING DATE:  12-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CONLIN, David G
;      REGISTRATION NUMBER:  27,026
;      REFERENCE/DOCKET NUMBER:  46509-DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  partial peptide
;      LOCATION:  1..34
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  11
;      OTHER INFORMATION:  /product= "Xaa=Ala(2-Naph)"
US-09-044-536A-12

  Query Match             58.0%;  Score 94;  DB 2;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 8.3e-05;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||       |  ||||||||||||||||
Db          1 SVSEIQLMHDXGKHLNSMERVEWLRKKLQDV 31


RESULT 11
US-09-843-221A-17
; Sequence 17, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-17

  Query Match             58.0%;  Score 94;  DB 2;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 8.3e-05;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||       |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 12
US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
```

```
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-18

  Query Match             58.0%;  Score 94;  DB 2;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 8.3e-05;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 13
US-09-843-221A-162
; Sequence 162, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162

  Query Match             58.0%;  Score 94;  DB 2;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 8.3e-05;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 14
US-09-843-221A-163
; Sequence 163, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HO
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163

  Query Match             58.0%;  Score 94;  DB 2;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 8.3e-05;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 15
US-08-142-551B-43
; Sequence 43, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  35
;      OTHER INFORMATION:  /note= "Where "Xaa" is selected
;      OTHER INFORMATION:  from the group consisting of Hol, Ho, a homoserine
;      OTHER INFORMATION:  amide, or the sequence of amino acids comprising
;      OTHER INFORMATION:  residues 35-84 of PTH."
US-08-142-551B-43

  Query Match             58.0%;  Score 94;  DB 1;  Length 35;
  Best Local Similarity   71.0%;  Pred. No. 8.6e-05;
  Matches   22;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||    | |  |||:|||||||||||||
Db          1 SVSEIQLLHGLGKHLNSLERVEWLRKKLQDV 31


Search completed: November 21, 2005, 16:16:22
Job time : 34 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:15:23 ; Search time 110.5 Seconds
(without alignments)
117.219 Million cell updates/sec

Title: US-09-475-158A-5
Perfect score: 162
Sequence: 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	104	64.2	89	5	US-10-997-078-132	Sequence 132, App
2	103	63.6	91	5	US-10-997-762-19	Sequence 19, Appl
3	103	63.6	91	5	US-10-997-822-4	Sequence 4, Appli
4	103	63.6	141	5	US-10-997-762-21	Sequence 21, Appl
5	95	58.6	33	4	US-10-361-928-6	Sequence 6, Appli
6	95	58.6	34	4	US-10-361-928-5	Sequence 5, Appli
7	94	58.0	31	5	US-10-892-025-20	Sequence 20, Appl
8	94	58.0	34	3	US-09-843-221A-17	Sequence 17, Appl
9	94	58.0	34	3	US-09-843-221A-18	Sequence 18, Appl
10	94	58.0	34	3	US-09-843-221A-162	Sequence 162, App
11	94	58.0	34	3	US-09-843-221A-163	Sequence 163, App
12	94	58.0	34	3	US-09-999-608-17	Sequence 17, Appl
13	94	58.0	34	3	US-09-999-608-18	Sequence 18, Appl
14	94	58.0	34	3	US-09-999-608-162	Sequence 162, App
15	94	58.0	34	3	US-09-999-608-163	Sequence 163, App
16	94	58.0	34	4	US-10-839-037-17	Sequence 17, Appl
17	94	58.0	34	4	US-10-839-037-18	Sequence 18, Appl
18	94	58.0	34	4	US-10-839-037-162	Sequence 162, App
19	94	58.0	34	4	US-10-839-037-163	Sequence 163, App
20	93	57.4	31	5	US-10-892-025-21	Sequence 21, Appl
21	93	57.4	31	5	US-10-892-025-22	Sequence 22, Appl
22	92	56.8	31	3	US-09-169-786-2	Sequence 2, Appli
23	92	56.8	31	3	US-09-843-221A-27	Sequence 27, Appl
24	92	56.8	31	3	US-09-843-221A-165	Sequence 165, App
25	92	56.8	31	3	US-09-999-608-27	Sequence 27, Appl
26	92	56.8	31	3	US-09-999-608-165	Sequence 165, App
27	92	56.8	31	4	US-10-440-473-2	Sequence 2, Appli
28	92	56.8	31	4	US-10-839-037-27	Sequence 27, Appl
29	92	56.8	31	4	US-10-839-037-165	Sequence 165, App
30	92	56.8	31	5	US-10-892-025-1	Sequence 1, Appli
31	92	56.8	31	6	US-11-066-697-271	Sequence 271, App
32	92	56.8	31	6	US-11-040-557-2	Sequence 2, Appli
33	92	56.8	32	5	US-10-892-025-2	Sequence 2, Appli
34	92	56.8	32	6	US-11-040-557-20	Sequence 20, Appl
35	92	56.8	33	4	US-10-361-928-9	Sequence 9, Appli
36	92	56.8	33	5	US-10-892-025-3	Sequence 3, Appli
37	92	56.8	33	6	US-11-040-557-1	Sequence 1, Appli
38	92	56.8	33	6	US-11-040-557-21	Sequence 21, Appl
39	92	56.8	34	3	US-09-169-786-3	Sequence 3, Appli
40	92	56.8	34	3	US-09-858-880-5	Sequence 5, Appli
41	92	56.8	34	3	US-09-928-047B-6	Sequence 6, Appli
42	92	56.8	34	3	US-09-843-221A-16	Sequence 16, Appl
43	92	56.8	34	3	US-09-843-221A-161	Sequence 161, App
44	92	56.8	34	3	US-09-928-048A-6	Sequence 6, Appli
45	92	56.8	34	3	US-09-999-608-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-10-997-078-132
; Sequence 132, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
; APPLICANT: Restoragen, Inc.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
; FILE REFERENCE: 1627.010US1
; CURRENT APPLICATION NUMBER: US/10/997,078
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16643
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,370
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic sequence for the T7tagVg-PTH(1-34) cassette.
US-10-997-078-132

Query Match 64.2%; Score 104; DB 5; Length 89;
Best Local Similarity 59.0%; Pred. No. 6.7e-05;
Matches 23; Conservative 1; Mismatches 3; Indels 12; Gaps 1;

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Qy          5 IGGGGGG----------GGGLNSMERVEWLRKKLQDV 31
              :|||||          | ||||||||||||||||||
Db         48 VGGGGGPRSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 86
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RESULT 2
US-10-997-762-19
; Sequence 19, Application US/10997762
; Publication No. US20050227313A1
; GENERAL INFORMATION:
; APPLICANT: Seo, Jin Seog
; APPLICANT: Strydom, Daniel
; APPLICANT: Holmquist, Barton
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Polypeptide Cleavage Process
; FILE REFERENCE: 1627.026US1
; CURRENT APPLICATION NUMBER: US/10/997,762
; CURRENT FILING DATE: 2004-11-24

```
;  PRIOR APPLICATION NUMBER: PCT/US03/16468
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,488
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 91
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic chimeric protein
US-10-997-762-19

  Query Match             63.6%;  Score 103;  DB 5;  Length 91;
  Best Local Similarity   56.1%;  Pred. No. 9e-05;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels   14;  Gaps    1;

Qy          5 IGGGGGG--------------GGGLNSMERVEWLRKKLQDV 31
              :|||||               |  ||||||||||||||||
Db         48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88


RESULT 3
US-10-997-822-4
; Sequence 4, Application US/10997822
; Publication No. US20050227314A1
; GENERAL INFORMATION:
;  APPLICANT: Holmquist, B.
;  APPLICANT:  Strydom, D.
;  APPLICANT:  Gensalk, X.
;  APPLICANT:  Cryer, R.
;  TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
;  FILE REFERENCE: 1627.011US1
;  CURRENT APPLICATION NUMBER: US/10/997,822
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16647
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,484
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 91
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of a synthetic chimeric protein.
US-10-997-822-4

  Query Match             63.6%;  Score 103;  DB 5;  Length 91;
  Best Local Similarity   56.1%;  Pred. No. 9e-05;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels   14;  Gaps    1;

Qy          5 IGGGGGG--------------GGGLNSMERVEWLRKKLQDV 31
              :|||||               |  ||||||||||||||||
Db         48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88


RESULT 4
US-10-997-762-21
; Sequence 21, Application US/10997762
; Publication No. US20050227313A1
; GENERAL INFORMATION:
;  APPLICANT: Seo, Jin Seog
;  APPLICANT:  Strydom, Daniel
;  APPLICANT:  Holmquist, Barton
;  APPLICANT:  Restoragen Inc.
;  TITLE OF INVENTION: Polypeptide Cleavage Process
;  FILE REFERENCE: 1627.026US1
;  CURRENT APPLICATION NUMBER: US/10/997,762
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16468
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,488
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic chimeric protein
US-10-997-762-21

  Query Match             63.6%;  Score 103;  DB 5;  Length 141;
  Best Local Similarity   56.1%;  Pred. No. 0.00014;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels   14;  Gaps    1;

Qy          5 IGGGGGG--------------GGGLNSMERVEWLRKKLQDV 31
              :|||||               |  ||||||||||||||||
Db         48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88


RESULT 5
US-10-361-928-6
; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT:  TAKASU, HISASHI
;  APPLICANT:  GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION:  ANALOGS
;  FILE REFERENCE: 0609.4630002
;  CURRENT APPLICATION NUMBER: US/10/361,928
;  CURRENT FILING DATE:  2003-02-11
;  PRIOR APPLICATION NUMBER: 09/447,800
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: 60/110,152
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-10-361-928-6

  Query Match             58.6%;  Score 95;  DB 4;  Length 33;
  Best Local Similarity   74.2%;  Pred. No. 0.00031;
  Matches   23;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||       |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 6
US-10-361-928-5
; Sequence 5, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT:  TAKASU, HISASHI
;  APPLICANT:  GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION:  ANALOGS
;  FILE REFERENCE: 0609.4630002
;  CURRENT APPLICATION NUMBER: US/10/361,928
;  CURRENT FILING DATE:  2003-02-11
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;  PRIOR APPLICATION NUMBER: 09/447,800
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: 60/110,152
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-10-361-928-5

  Query Match             58.6%;  Score 95;  DB 4;  Length 34;
  Best Local Similarity   74.2%;  Pred. No. 0.00032;
  Matches   23;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              |||||      |  ||||||||||||||||
Db          1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 7
US-10-892-025-20
; Sequence 20, Application US/10892025
; Publication No. US20050065071A1
; GENERAL INFORMATION:
;  APPLICANT: Morley, Paul
;  APPLICANT:  Whitfield, James F
;  TITLE OF INVENTION: CYCLIC ANALOGS OF HUMAN PARATHYROID
;  TITLE OF INVENTION:  HORMONE FOR THE TREATMENT OF CONDITIONS CHARACTERIZED BY
;  TITLE OF INVENTION:  HYPERPROLIFERATIVE SKIN CELLS
;  FILE REFERENCE: 3583.1000-001
;  CURRENT APPLICATION NUMBER: US/10/892,025
;  CURRENT FILING DATE:  2004-07-15
;  PRIOR APPLICATION NUMBER: 60/487,513
;  PRIOR FILING DATE: 2003-07-15
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 1
;   OTHER INFORMATION: NHR; wherein R is hydrogen or a linear or branched
;   OTHER INFORMATION: chain alkyl, acyl or aryl group
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 8
;   OTHER INFORMATION: is selected from the group consisting of Met,
;   OTHER INFORMATION: norisoleucine, and a hydrophobic amino acid
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 31
;   OTHER INFORMATION: Y; where Y is X, His-X, His-Asn-X, or
;   OTHER INFORMATION: His-Asn-Phe-X; where X is OR or NHR; and R is
;   OTHER INFORMATION: hydrogen or a linear or branched chain alkyl, acyl
;   OTHER INFORMATION: or aryl group
US-10-892-025-20

  Query Match             58.0%;  Score 94;  DB 5;  Length 31;
  Best Local Similarity   71.0%;  Pred. No. 0.00039;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||
Db          1 SVSEIQLXHNLGKHLNSMERVEWLRKKLQDV 31


RESULT 8
US-09-843-221A-17
; Sequence 17, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-17

  Query Match             58.0%;  Score 94;  DB 3;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 0.00042;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 9
US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-18

  Query Match             58.0%;  Score 94;  DB 3;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 0.00042;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
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              :||||      |  ||||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 10
US-09-843-221A-162
; Sequence 162, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162

  Query Match             58.0%;  Score 94;  DB 3;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 0.00042;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 11
US-09-843-221A-163
; Sequence 163, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
;   NAME/KEY: misc_feature
;   LOCATION: (34)..(34)
;   OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163

  Query Match             58.0%;  Score 94;  DB 3;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 0.00042;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||||
Db          1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31


RESULT 12
US-09-999-608-17
; Sequence 17, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  GEGG, COLIN V.
;  APPLICANT:  JAROSINSKI, MARK ANTHONY
;  APPLICANT:  KINSTLER, OLAF BORIS
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
;  TITLE OF INVENTION:  HORMONE-RELATED PROTEIN
;  FILE REFERENCE: A-665C
;  CURRENT APPLICATION NUMBER: US/09/999,608
;  CURRENT FILING DATE:  2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/843,221
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: US 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: US 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modifiied human PTH
US-09-999-608-17

  Query Match             58.0%;  Score 94;  DB 3;  Length 34;
  Best Local Similarity   71.0%;  Pred. No. 0.00042;
  Matches   22;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
              :||||      |  ||||||||||||||||||
Db          1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31


RESULT 13
US-09-999-608-18
; Sequence 18, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  GEGG, COLIN V.
;  APPLICANT:  JAROSINSKI, MARK ANTHONY
;  APPLICANT:  KINSTLER, OLAF BORIS
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
;  TITLE OF INVENTION:  HORMONE-RELATED PROTEIN
;  FILE REFERENCE: A-665C
;  CURRENT APPLICATION NUMBER: US/09/999,608
;  CURRENT FILING DATE:  2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/843,221
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: US 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/214,860
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; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-999-608-18

Query Match 58.0%; Score 94; DB 3; Length 34;
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
:|||| | ||||||||||||||||||
Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31

RESULT 14
US-09-999-608-162
; Sequence 162, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: GEGG, COLIN V.
; APPLICANT: JAROSINSKI, MARK ANTHONY
; APPLICANT: KINSTLER, OLAF BORIS
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN
; FILE REFERENCE: A-665C
; CURRENT APPLICATION NUMBER: US/09/999,608
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-999-608-162

Query Match 58.0%; Score 94; DB 3; Length 34;
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
:|||| | ||||||||||||||||||
Db 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31

RESULT 15
US-09-999-608-163
; Sequence 163, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: GEGG, COLIN V.
; APPLICANT: JAROSINSKI, MARK ANTHONY
; APPLICANT: KINSTLER, OLAF BORIS
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN
; FILE REFERENCE: A-665C
; CURRENT APPLICATION NUMBER: US/09/999,608
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-999-608-163

Query Match 58.0%; Score 94; DB 3; Length 34;
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31
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Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31

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Job time : 110.5 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

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Title: US-09-475-158A-5
Perfect score: 162
Sequence: 1 AVSEIGGGGGGGGGLNSMERVEWLRKKLQDV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	68.5	42.3	1493	7	US-11-004-057-4	Sequence 4, Appli
2	60	37.0	579	1	US-10-975-798-4	Sequence 4, Appli
3	60	37.0	580	1	US-10-975-798-3	Sequence 3, Appli
4	56.5	34.9	1493	7	US-11-004-057-21	Sequence 21, Appl
5	54	33.3	157	1	US-10-957-569-64	Sequence 64, Appl
6	54	33.3	200	1	US-10-841-129-7	Sequence 7, Appli
7	54	33.3	200	7	US-11-060-659-32	Sequence 32, Appl
8	54	33.3	269	1	US-10-131-826A-532	Sequence 532, App
9	54	33.3	562	7	US-11-065-943-20	Sequence 20, Appl
10	54	33.3	562	7	US-11-065-943-22	Sequence 22, Appl
11	54	33.3	562	7	US-11-065-943-24	Sequence 24, Appl
12	54	33.3	562	7	US-11-065-943-26	Sequence 26, Appl
13	54	33.3	562	7	US-11-065-943-28	Sequence 28, Appl
14	54	33.3	562	7	US-11-065-943-30	Sequence 30, Appl
15	54	33.3	562	7	US-11-065-943-32	Sequence 32, Appl
16	54	33.3	562	7	US-11-065-943-34	Sequence 34, Appl
17	54	33.3	562	7	US-11-065-943-36	Sequence 36, Appl
18	54	33.3	562	7	US-11-065-943-38	Sequence 38, Appl
19	51	31.5	327	1	US-10-512-184-64	Sequence 64, Appl
20	51	31.5	1127	7	US-11-077-550-40	Sequence 40, Appl
21	51	31.5	1127	7	US-11-077-550-50	Sequence 50, Appl
22	51	31.5	1127	7	US-11-077-550-54	Sequence 54, Appl
23	51	31.5	1127	7	US-11-077-550-58	Sequence 58, Appl
24	51	31.5	1130	7	US-11-077-550-44	Sequence 44, Appl
25	49	30.2	888	1	US-10-131-826A-544	Sequence 544, App
26	48	29.6	10	1	US-10-512-184-44	Sequence 44, Appl
27	48	29.6	15	1	US-10-495-664-1	Sequence 1, Appli
28	48	29.6	15	1	US-10-967-457-72	Sequence 72, Appl
29	48	29.6	15	1	US-10-839-799-111	Sequence 111, App
30	48	29.6	15	7	US-11-144-248-60	Sequence 60, Appl
31	48	29.6	20	7	US-11-065-943-48	Sequence 48, Appl
32	48	29.6	248	1	US-10-512-184-32	Sequence 32, Appl
33	48	29.6	251	1	US-10-512-184-30	Sequence 30, Appl
34	48	29.6	259	1	US-10-512-184-31	Sequence 31, Appl
35	48	29.6	259	1	US-10-512-184-33	Sequence 33, Appl
36	48	29.6	269	1	US-10-839-799-109	Sequence 109, App
37	48	29.6	313	1	US-10-512-184-72	Sequence 72, Appl
38	48	29.6	317	1	US-10-512-184-69	Sequence 69, Appl
39	48	29.6	320	1	US-10-512-184-67	Sequence 67, Appl
40	48	29.6	327	1	US-10-512-184-62	Sequence 62, Appl
41	48	29.6	328	1	US-10-512-184-63	Sequence 63, Appl
42	48	29.6	329	1	US-10-512-184-68	Sequence 68, Appl
43	48	29.6	329	1	US-10-512-184-70	Sequence 70, Appl
44	48	29.6	371	1	US-10-512-184-71	Sequence 71, Appl
45	48	29.6	465	1	US-10-967-648A-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-11-004-057-4
; Sequence 4, Application US/11004057
; Publication No. US20050244846A1
; GENERAL INFORMATION:
;  APPLICANT: Johnson, Gary L.
;  TITLE OF INVENTION: MEKK1 PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING
;  TITLE OF INVENTION:  APOPTOSIS
;  FILE REFERENCE: CPI-042CPPC
;  CURRENT APPLICATION NUMBER: US/11/004,057
;  CURRENT FILING DATE:  2004-12-02
;  PRIOR APPLICATION NUMBER: US/09/403,075
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1493
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-004-057-4

  Query Match             42.3%;  Score 68.5;  DB 7;  Length 1493;
  Best Local Similarity   32.0%;  Pred. No. 0.063;
  Matches   16;  Conservative    4;  Mismatches   11;  Indels   19;  Gaps    1;

Qy          1 AVSEIGGGGGGGGGLN------------------SMERVEWLRKKLQDV 31
              |  | |||||||| |                  || :| |: :: |
Db         20 ASPEAGGGGGGGGALQGSGAPAAGAAGLLREPGSAGRERADWRRRHVRKV 69


RESULT 2
US-10-975-798-4
; Sequence 4, Application US/10975798
; Publication No. US20050250090A1
; GENERAL INFORMATION:
;  APPLICANT: Edward Kaftan
;  APPLICANT:  Adrienne Dubin
;  APPLICANT:  Sandy Chaplan
;  TITLE OF INVENTION: ASSAY SYSTEMS AND METHODS FOR DETECTING MOLECULES THAT INTERACT
;  TITLE OF INVENTION:  WITH SK2 CHANNELS
;  FILE REFERENCE: PRD2142
;  CURRENT APPLICATION NUMBER: US/10/975,798
;  CURRENT FILING DATE:  2004-10-28
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 579
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-10-975-798-4

  Query Match             37.0%;  Score 60;  DB 1;  Length 579;
  Best Local Similarity   46.2%;  Pred. No. 0.27;
  Matches   12;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVEWLRKKLQDV 31
              ||||||| |  |    :  :|| |::
Db         92 GGGGGGGSGHGSSSGTKSSKKKNQNI 117


RESULT 3
US-10-975-798-3
; Sequence 3, Application US/10975798
; Publication No. US20050250090A1
; GENERAL INFORMATION:
;  APPLICANT: Edward Kaftan
;  APPLICANT:  Adrienne Dubin
;  APPLICANT:  Sandy Chaplan
;  TITLE OF INVENTION: ASSAY SYSTEMS AND METHODS FOR DETECTING MOLECULES THAT INTERACT
;  TITLE OF INVENTION:  WITH SK2 CHANNELS
;  FILE REFERENCE: PRD2142
;  CURRENT APPLICATION NUMBER: US/10/975,798
;  CURRENT FILING DATE:  2004-10-28
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 580
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-975-798-3

  Query Match             37.0%;  Score 60;  DB 1;  Length 580;
  Best Local Similarity   46.2%;  Pred. No. 0.27;
  Matches   12;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVEWLRKKLQDV 31
              ||||||| |  |    :  :|| |::
Db         93 GGGGGGGSGHGSSSGTKSSKKKNQNI 118


RESULT 4
US-11-004-057-21
; Sequence 21, Application US/11004057
; Publication No. US20050244846A1
; GENERAL INFORMATION:
;  APPLICANT: Johnson, Gary L.
;  TITLE OF INVENTION: MEKK1 PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING
;  TITLE OF INVENTION:  APOPTOSIS
;  FILE REFERENCE: CPI-042CPPC
;  CURRENT APPLICATION NUMBER: US/11/004,057
;  CURRENT FILING DATE:  2004-12-02
;  PRIOR APPLICATION NUMBER: US/09/403,075
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 1493
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-11-004-057-21

  Query Match             34.9%;  Score 56.5;  DB 7;  Length 1493;
  Best Local Similarity   34.8%;  Pred. No. 1.8;
  Matches   16;  Conservative    4;  Mismatches   11;  Indels   15;  Gaps    2;

Qy          1 AVSEIGGGGG----------GGG-----GLNSMERVEWLRKKLQDV 31
              | | |||||          |||     |    || :| |::|: |
Db         20 ASPEAGGGGGALQGSGAPAAGAGLLRETGSAGRERADWRRQQLRKV 65


RESULT 5
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US-10-957-569-64
; Sequence 64, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
;  APPLICANT: COOK, Zhihong et al.
;  TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2750-1577PUS3
;  CURRENT APPLICATION NUMBER: US/10/957,569
;  CURRENT FILING DATE:  2004-09-30
;  PRIOR APPLICATION NUMBER: US 10/950,321
;  PRIOR FILING DATE: 2004-09-23
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-957-569-64

  Query Match             33.3%;  Score 54;  DB 1;  Length 157;
  Best Local Similarity   42.9%;  Pred. No. 0.39;
  Matches   12;  Conservative    2;  Mismatches    6;  Indels    8;  Gaps    1;

Qy          6 GGGG--------GGGGGLNSMERVEWLR 25
              ||||        ||||| :|    :| |
Db         76 GGGGARSGGRSRGGGGGSSSSRSRDWKR 103


RESULT 6
US-10-841-129-7
; Sequence 7, Application US/10841129
; Publication No. US20050250113A1
; GENERAL INFORMATION:
;  APPLICANT: Zuker, Charles S.
;  APPLICANT:  Erlenbach, Isolda
;  APPLICANT:  Hoon, Mark A.
;  APPLICANT:  Ryba, Nicholas J. P.
;  APPLICANT:  Zhang, Yifeng
;  APPLICANT:  The Regents of the University of California
;  APPLICANT:  The Government of the United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: A Mammalian Magnesium/Manganese Sensing G Protein
;  TITLE OF INVENTION:  Coupled Receptor
;  FILE REFERENCE: 02307E-145400US
;  CURRENT APPLICATION NUMBER: US/10/841,129
;  CURRENT FILING DATE:  2004-05-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 200
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:poly Gly
;   OTHER INFORMATION: flexible linker
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (6)..(200)
;   OTHER INFORMATION: Gly residues from position 6 to 200 may be present
;   OTHER INFORMATION: or absent
US-10-841-129-7

  Query Match             33.3%;  Score 54;  DB 1;  Length 200;
  Best Local Similarity   100.0%;  Pred. No. 0.49;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGG 14
              |||||||||
Db          1 GGGGGGGGG 9
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RESULT 7
US-11-060-659-32
; Sequence 32, Application US/11060659
; Publication No. US20050250163A1
; GENERAL INFORMATION:
;  APPLICANT: Lorens, James
;  APPLICANT:  Holland, Sacha J.
;  APPLICANT:  Xu, Weiduan
;  APPLICANT:  Rigel Pharmaceuticals, Incorporated
;  TITLE OF INVENTION: Modulators of Angiogenesis and Tumorigenesis
;  FILE REFERENCE: 021044-008310US
;  CURRENT APPLICATION NUMBER: US/11/060,659
;  CURRENT FILING DATE:  2005-02-16
;  PRIOR APPLICATION NUMBER: US 60/545,981
;  PRIOR FILING DATE: 2004-02-17
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
;  TITLE OF INVENTION: ), SH3 domain-binding protein 2
;  TITLE OF INVENTION:  (KIAA0660) cDNA
;  TITLE OF INVENTION: ), SH3 domain-binding protein 2
;  TITLE OF INVENTION:  (KIAA0660) cDNA
; SEQ ID NO 32
;   LENGTH: 200
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic poly
;   OTHER INFORMATION: Gly flexible linker
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (6)..(200)
;   OTHER INFORMATION: Gly residues from position 6 to 200 may be present
;   OTHER INFORMATION: or absent
US-11-060-659-32

  Query Match             33.3%;  Score 54;  DB 7;  Length 200;
  Best Local Similarity   100.0%;  Pred. No. 0.49;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGG 14
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Db          1 GGGGGGGGG 9


RESULT 8
US-10-131-826A-532
; Sequence 532, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C128
;  CURRENT APPLICATION NUMBER: US/10/131,826A
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 532
;   LENGTH: 269
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-131-826A-532

  Query Match             33.3%;  Score 54;  DB 1;  Length 269;
  Best Local Similarity   100.0%;  Pred. No. 0.66;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGG 14
              |||||||||
Db        249 GGGGGGGGG 257


RESULT 9
US-11-065-943-20
; Sequence 20, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
;  APPLICANT: JESTIN, JEAN-LUC
;  APPLICANT:  VICHIER-GUERRE, SOPHIE
;  APPLICANT:  FERRIS, STEPHANE
;  TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
;  TITLE OF INVENTION:  VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
;  TITLE OF INVENTION:  METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
;  FILE REFERENCE: 266426US0XCIP
;  CURRENT APPLICATION NUMBER: US/11/065,943
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 10/787,219
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Thermus aquaticus
US-11-065-943-20

  Query Match             33.3%;  Score 54;  DB 7;  Length 562;
  Best Local Similarity   50.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVEW 23
              ||| ||||   ::|   |
Db          5 GGGCGGGGSPKALEEAPW 22


RESULT 10
US-11-065-943-22
; Sequence 22, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: JESTIN, JEAN-LUC
;  APPLICANT:  VICHIER-GUERRE, SOPHIE
;  APPLICANT:  FERRIS, STEPHANE
;  TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
;  TITLE OF INVENTION:  VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
;  TITLE OF INVENTION:  METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
;  FILE REFERENCE: 266426US0XCIP
;  CURRENT APPLICATION NUMBER: US/11/065,943
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 10/787,219
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Thermus aquaticus
US-11-065-943-22

  Query Match             33.3%;  Score 54;  DB 7;  Length 562;
  Best Local Similarity   50.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVEW 23
              ||| ||||   ::|   |
Db          5 GGGCGGGGSPKALEEAPW 22


RESULT 11
US-11-065-943-24
; Sequence 24, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
;  APPLICANT: JESTIN, JEAN-LUC
;  APPLICANT:  VICHIER-GUERRE, SOPHIE
;  APPLICANT:  FERRIS, STEPHANE
;  TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
;  TITLE OF INVENTION:  VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
;  TITLE OF INVENTION:  METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
;  FILE REFERENCE: 266426US0XCIP
;  CURRENT APPLICATION NUMBER: US/11/065,943
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 10/787,219
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Thermus aquaticus
US-11-065-943-24

  Query Match             33.3%;  Score 54;  DB 7;  Length 562;
  Best Local Similarity   50.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVEW 23
              ||| ||||   ::|   |
Db          5 GGGCGGGGSPKALEEAPW 22


RESULT 12
US-11-065-943-26
; Sequence 26, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
;  APPLICANT: JESTIN, JEAN-LUC
;  APPLICANT:  VICHIER-GUERRE, SOPHIE
;  APPLICANT:  FERRIS, STEPHANE
;  TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
;  TITLE OF INVENTION:  VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
;  TITLE OF INVENTION:  METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
;  FILE REFERENCE: 266426US0XCIP
;  CURRENT APPLICATION NUMBER: US/11/065,943
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 10/787,219
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Thermus aquaticus
US-11-065-943-26

  Query Match             33.3%;  Score 54;  DB 7;  Length 562;
  Best Local Similarity   50.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVEW 23
              ||| ||||   ::|   |
Db          5 GGGCGGGGSPKALEEAPW 22


RESULT 13
US-11-065-943-28
; Sequence 28, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
;  APPLICANT: JESTIN, JEAN-LUC
;  APPLICANT:  VICHIER-GUERRE, SOPHIE
;  APPLICANT:  FERRIS, STEPHANE
;  TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
;  TITLE OF INVENTION:  VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
;  TITLE OF INVENTION:  METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
;  FILE REFERENCE: 266426US0XCIP
;  CURRENT APPLICATION NUMBER: US/11/065,943
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 10/787,219
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Thermus aquaticus
US-11-065-943-28

  Query Match             33.3%;  Score 54;  DB 7;  Length 562;
  Best Local Similarity   50.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVEW 23
              ||| ||||   ::|   |
Db          5 GGGCGGGGSPKALEEAPW 22


RESULT 14
US-11-065-943-30
; Sequence 30, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
;  APPLICANT: JESTIN, JEAN-LUC
;  APPLICANT:  VICHIER-GUERRE, SOPHIE
;  APPLICANT:  FERRIS, STEPHANE
;  TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
;  TITLE OF INVENTION:  VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
;  TITLE OF INVENTION:  METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
;  FILE REFERENCE: 266426US0XCIP
;  CURRENT APPLICATION NUMBER: US/11/065,943
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 10/787,219
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
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;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Thermus aquaticus
US-11-065-943-30

  Query Match             33.3%;  Score 54;  DB 7;  Length 562;
  Best Local Similarity   50.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVEW 23
              ||| ||||   ::|   |
Db          5 GGGCGGGGSPKALEEAPW 22


RESULT 15
US-11-065-943-32
; Sequence 32, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
;  APPLICANT: JESTIN, JEAN-LUC
;  APPLICANT:  VICHIER-GUERRE, SOPHIE
;  APPLICANT:  FERRIS, STEPHANE
;  TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
;  TITLE OF INVENTION:  VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
;  TITLE OF INVENTION:  METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
;  FILE REFERENCE: 266426US0XCIP
;  CURRENT APPLICATION NUMBER: US/11/065,943
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 10/787,219
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Thermus aquaticus
US-11-065-943-32

  Query Match             33.3%;  Score 54;  DB 7;  Length 562;
  Best Local Similarity   50.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 GGGGGGGGGLNSMERVEW 23
              ||| ||||   ::|   |
Db          5 GGGCGGGGSPKALEEAPW 22


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Job time : 4.5 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:00:32 ; Search time 242.667 Seconds
(without alignments)
2554.189 Million cell updates/sec

Title: US-09-475-158A-14
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	93	3	AAA51729	Aaa51729 PTH funct
2	83.4	89.7	93	3	AAA51730	Aaa51730 PTH funct
3	73.8	79.4	93	3	AAA51731	Aaa51731 PTH funct
4	71.2	76.6	152	2	AAT73910	Aat73910 Synthetic
5	69.6	74.8	102	12	ADG93179	Adg93179 Novel exp
6	69.6	74.8	102	12	ADJ65857	Adj65857 PTH pepti
7	69.6	74.8	102	13	ADW14377	Adw14377 Human par
8	69.6	74.8	111	12	ADG93180	Adg93180 Novel exp
9	69.6	74.8	111	12	ADJ65858	Adj65858 PTH pepti
10	69.6	74.8	111	13	ADW14375	Adw14375 Human par
11	69.6	74.8	117	12	ADG93260	Adg93260 Novel exp
12	69.6	74.8	168	2	AAT34865	Aat34865 Plasmid p
13	69.6	74.8	252	12	ADG93181	Adg93181 Novel exp
14	69.6	74.8	252	12	ADJ65859	Adj65859 PTH prote
15	69.6	74.8	264	12	ADJ65913	Adj65913 Tandem po
16	69.6	74.8	276	12	ADF90345	Adf90345 Chimeric
17	69.6	74.8	276	12	ADJ65899	Adj65899 PTH DNA s
18	69.6	74.8	276	12	ADJ87051	Adj87051 Nucleotid
19	69.6	74.8	282	12	ADG93252	Adg93252 Novel exp
20	69.6	74.8	291	12	ADJ65901	Adj65901 PTH DNA s
21	69.6	74.8	291	12	ADJ65900	Adj65900 PTH DNA s
22	69.6	74.8	294	2	AAT34866	Aat34866 Plasmid p
23	69.6	74.8	321	12	ADJ65915	Adj65915 Tandem po
24	69.6	74.8	420	12	ADJ65917	Adj65917 Tandem po
25	69.6	74.8	426	12	ADF90347	Adf90347 Chimeric
26	69.6	74.8	528	6	AAS19702	Aas19702 DNA encod
27	68	73.1	108	13	ADV69494	Adv69494 Human par
28	68	73.1	114	13	ADV69502	Adv69502 Human par
29	68	73.1	489	12	ADG48030	Adg48030 Human PTH
30	68	73.1	489	12	ADG48059	Adg48059 Human PTH
31	68	73.1	489	12	ADG68786	Adg68786 Human mut
32	63.8	68.6	141	2	AAQ89920	Aaq89920 Recombina
33	63.8	68.6	141	2	AAT80383	Aat80383 rPTH codi
34	63.8	68.6	207	2	AAQ89923	Aaq89923 Expressio
35	62.2	66.9	145	13	ADW80822	Adw80822 DNA encod
36	60	64.5	405	3	AAA51452	Aaa51452 PCpB-RVR-
37	60	64.5	408	3	AAA51455	Aaa51455 PCpB-LVPR
38	60	64.5	408	3	AAA51454	Aaa51454 PCpB-IEGR
39	60	64.5	411	3	AAA51453	Aaa51453 PCpB-ALY-
40	60	64.5	414	3	AAA51459	Aaa51459 PCpB-APR-
41	60	64.5	417	3	AAA51456	Aaa51456 PCpB-VIPR
42	60	64.5	423	3	AAA51457	Aaa51457 PCpB-DQVD
43	60	64.5	435	3	AAA51458	Aaa51458 PCpB-DFIA
44	57.4	61.7	728	2	AAQ55301	Aaq55301 Truncated
45	57.4	61.7	945	2	AAQ55302	Aaq55302 gp55-Asn-

ALIGNMENTS

RESULT 1
AAA51729
ID AAA51729 standard; RNA; 93 BP.
XX
AC AAA51729;
XX
DT 31-OCT-2000 (first entry)
XX
DE PTH functional domain conjugate peptide PG5 coding sequence.
XX
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW resorption; remodeling; tether1; osteoporosis; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .93
FT /*tag= a
FT /product= "PG5"
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
DR P-PSDB; AAY96973.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.

XX
PS Claim 14; Fig 1; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 93 BP; 21 A; 18 C; 30 G; 0 T; 24 U; 0 Other;

Query Match 100.0%; Score 93; DB 3; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-22;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60

Qy 61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
|||||||||||||||||||||||||||||||||
Db 61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93

RESULT 2
AAA51730
ID AAA51730 standard; RNA; 93 BP.
XX
AC AAA51730;
XX
DT 31-OCT-2000 (first entry)
XX
DE PTH functional domain conjugate peptide PG7 coding sequence.
XX
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW resorption; remodeling; tether1; osteoporosis; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .93
FT /*tag= a
FT /product= "PG7"
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
DR P-PSDB; AAY96975.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 14; Fig 1; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 93 BP; 19 A; 16 C; 33 G; 0 T; 25 U; 0 Other;

Query Match 89.7%; Score 83.4; DB 3; Length 93;
Best Local Similarity 93.5%; Pred. No. 2.5e-19;
Matches 87; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
|||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db 1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60

Qy 61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
|||||||||||||||||||||||||||||||||
Db 61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93

RESULT 3
AAA51731
ID AAA51731 standard; RNA; 93 BP.
XX
AC AAA51731;
XX
DT 31-OCT-2000 (first entry)
XX
DE PTH functional domain conjugate peptide PG9 coding sequence.
XX
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW resorption; remodeling; tether1; osteoporosis; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .93
FT /*tag= a
FT /product= "PG9"
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
DR P-PSDB; AAY96974.

XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 14; Fig 1; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 93 BP; 18 A; 14 C; 35 G; 0 T; 26 U; 0 Other;

Query Match 79.4%; Score 73.8; DB 3; Length 93;
Best Local Similarity 87.1%; Pred. No. 6e-16;
Matches 81; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```
Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||||||||||||||||           ||||||||||||||||||||||||||||||||
Db          1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ||||||||||||||||||||||||||||||||
Db         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
```

RESULT 4
AAT73910
ID AAT73910 standard; DNA; 152 BP.
XX
AC AAT73910;
XX
DT 25-MAR-2003 (revised)
DT 30-JAN-1998 (first entry)
XX
DE Synthetic oligonucleotide encoding linker and PTH 1-37.
XX
KW Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein;
KW recombinant production; endoproteinase LysC; ds.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .4
FT /*tag= b
FT /label= sticky_end
FT /note= "5' end of complementary strand overhangs 3' end
FT of present strand by sequence 5'-TCGA-3'"
FT CDS 6. .152
FT /*tag= a
XX
PN WO9718314-A1.
XX
PD 22-MAY-1997.
XX
PF 06-NOV-1996; 96WO-EP004850.
XX
PR 16-NOV-1995; 95DE-01042702.
XX
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
XX
PI Kopetzki E;
XX
DR WPI; 1997-289290/26.
DR P-PSDB; AAW21946.
XX
PT Recombinant production of peptide(s) as fusions with streptavidin
PT attached via cleavable linker - especially for urotropin and parathyroid
PT hormone production.
XX
PS Example 2; Fig 2; 37pp; German.
XX
CC The present sequence, which encodes a linker and the parathyroid hormone
CC 1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was
CC ligated to the 2.9 kb NheI-HindIII fragment of pSAM-CORE, which contains
CC the Met(13-139) streptavidin (SA) sequence, to give pSA-EK-PTH. pSA-EK-
CC PTH and the LacIq repressor plasmid pUBS500 were used to transform E.
CC coli K12 RM82. The transformants were grown, with IPTG induction, in
CC medium containing kanamycin and ampilcilin. Cells were harvested, lysed
CC and isolated inclusion bodies solubilised in guanidine hydrochloride, and
CC renatured by dilution in pH 7 phosphate buffer. The solution was
CC clarified and the supernatant concentrated and purified on a column of
CC immobilised iminobiotin. The purified material was incubated with
CC endoproteinase LysC and the PTH 1-37 fragment released, recovered by SA
CC fragment removal on an iminobiotin column followed by chromatography on a
CC fractogel and reverse phase HPLC. The endoproteinase LysC cleaves the
CC fusion protein rapidly and completely, exclusively at the Lys residue in
CC the linker, i.e. not at Lys residues in SA. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;

Query Match 76.6%; Score 71.2; DB 2; Length 152;
Best Local Similarity 65.2%; Pred. No. 5.7e-15;
Matches 60; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

```
Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|||||:||:||||      ||:      |:||||:|||:||||||:|
Db         37 CCGTTTCCGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCCATGGAACGTG 96

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:||||||||:||||||||::
Db         97 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 128
```

RESULT 5
ADG93179
ID ADG93179 standard; DNA; 102 BP.
XX
AC ADG93179;
XX
DT 11-MAR-2004 (first entry)
XX
DE Novel expression cassette-related polypeptide-encoding DNA SeqID60.
XX
KW expression cassette; high yield polypeptide production;
KW tandem polypeptide; inclusion body; gene; ds.
XX
OS Unidentified.
XX
PN WO2003100021-A2.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-US016643.
XX
PR 24-MAY-2002; 2002US-0383370P.
XX
PA (REST-) RESTORAGEN INC.
PA (HARL/) HARLEY S.
XX
PI Harley S, Williams JA, Luan P, Xia Y;
XX
DR WPI; 2004-035128/03.

DR P-PSDB; ADG93159.
XX
PT New expression cassette comprising an operably linked nucleic acid
PT sequence, useful for producing a tandem polypeptide that forms an
PT inclusion body when expressed in a cell.
XX
PS Disclosure; SEQ ID NO 60; 157pp; English.
XX
CC This invention relates to a novel expression cassette and methods for
CC high yield production of polypeptides. The cassette comprises an operably
CC linked nucleic acid sequence, where the expression of the cassette
CC produces a tandem polypeptide that forms an inclusion body when expressed
CC in a cell. The expression cassette is useful for producing peptide and
CC polypeptide in a cell, preferably a tandem polypeptide that forms an
CC inclusion body when expressed in a cell. The present sequence is that of
CC a DNA sequence which encodes a polypeptide which may be produced using
CC the expression cassette of the invention.
XX
SQ Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

Query Match 74.8%; Score 69.6; DB 12; Length 102;
Best Local Similarity 63.0%; Pred. No. 1.9e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

Qy 2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
|:|:::| ||||:|||||:||:|||| ||: |:||||:| |:|||||:|
Db 2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||:||||||::
Db 62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93

RESULT 6
ADJ65857
ID ADJ65857 standard; DNA; 102 BP.
XX
AC ADJ65857;
XX
DT 06-MAY-2004 (first entry)
XX
DE PTH peptide coding sequence #1.
XX
KW expression cassette; tandem polypeptide; inclusion body;
KW inclusion body fusion partner; PTH; gene; ds.
XX
OS Unidentified.
XX
PN WO2003100022-A2.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-US016645.
XX
PR 24-MAY-2002; 2002US-0383212P.
XX
PA (REST-) RESTORAGEN INC.
XX
PI Xia Y, Peng L;
XX
DR WPI; 2004-035129/03.
DR P-PSDB; ADJ65837.
XX
PT New expression cassette comprising an operably linked nucleic acid
PT sequence, useful for producing a tandem polypeptide that forms an
PT inclusion body when expressed in a cell.
XX
PS Disclosure; SEQ ID NO 33; 132pp; English.
XX
CC The invention comprises an expression cassette which produces a tandem
CC polypeptide that form an inclusion body when expressed in a cell. The
CC expression cassette of the invention is useful for producing a peptide or
CC polypeptide in a cell, preferably a tandem polypeptide that forms an
CC inclusion body when expressed in a cell. The present DNA sequence encodes
CC a peptide which may be used in the construction of a tandem polypeptide
CC of the invention.
XX
SQ Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

Query Match 74.8%; Score 69.6; DB 12; Length 102;
Best Local Similarity 63.0%; Pred. No. 1.9e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

Qy 2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
|:|:::| ||||:|||||:||:|||| ||: |:||||:| |:|||||:|
Db 2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||:||||||::
Db 62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93

RESULT 7
ADW14377
ID ADW14377 standard; DNA; 102 BP.
XX
AC ADW14377;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human parathyroxin PTH 1-34 peptide encoding DNA SEQ ID NO:3.
XX
KW ds; parathyroxin; recombinant protein; protein engineering.
XX
OS Homo sapiens.
XX
PN CN1424325-A.
XX
PD 18-JUN-2003.
XX
PF 12-DEC-2001; 2001CN-00142627.
XX
PR 12-DEC-2001; 2001CN-00142627.
XX
PA (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.
XX
PI Chen C, Xiu C, Li M;
XX
DR WPI; 2004-099606/11.
DR P-PSDB; ADW14378.
XX
PT Production of reorganized human parathyroid hormone 1-34 peptide.
XX
PS Disclosure; SEQ ID NO 3; 25pp; Chinese.
XX
CC The invention relates to a novel process for preparing recombinant human
CC parathyroxin 1-34 peptide, including such steps as culturing a host cell
CC in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376),
CC severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and
CC separating and purifying PTH 1-34 peptide. The present sequence encodes
CC the PTH 1-34 peptide.
XX
SQ Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

Query Match 74.8%; Score 69.6; DB 13; Length 102;
Best Local Similarity 63.0%; Pred. No. 1.9e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

Qy 2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
|:|:::| ||||:|||||:||:|||| ||: |:||||:| |:|||||:|
Db 2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||:||||||::
Db 62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93

```
RESULT 8
ADG93180
ID   ADG93180 standard; DNA; 111 BP.
XX
AC   ADG93180;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel expression cassette-related polypeptide-encoding DNA SeqID61.
XX
KW   expression cassette; high yield polypeptide production;
KW   tandem polypeptide; inclusion body; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100021-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016643.
XX
PR   24-MAY-2002; 2002US-0383370P.
XX
PA   (REST-) RESTORAGEN INC.
PA   (HARL/) HARLEY S.
XX
PI   Harley S,  Williams JA,  Luan P,  Xia Y;
XX
DR   WPI; 2004-035128/03.
DR   P-PSDB; ADG93160.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 61; 157pp; English.
XX
CC   This invention relates to a novel expression cassette and methods for
CC   high yield production of polypeptides. The cassette comprises an operably
CC   linked nucleic acid sequence, where the expression of the cassette
CC   produces a tandem polypeptide that forms an inclusion body when expressed
CC   in a cell. The expression cassette is useful for producing peptide and
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present sequence is that of
CC   a DNA sequence which encodes a polypeptide which may be produced using
CC   the expression cassette of the invention.
XX
SQ   Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;

  Query Match             74.8%;  Score 69.6;  DB 12;  Length 111;
  Best Local Similarity   63.0%;  Pred. No. 1.9e-14;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 9
ADJ65858
ID   ADJ65858 standard; DNA; 111 BP.
XX
AC   ADJ65858;
XX
DT   06-MAY-2004  (first entry)
XX
DE   PTH peptide coding sequence #2.
XX
KW   expression cassette; tandem polypeptide; inclusion body;
KW   inclusion body fusion partner; PTH; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100022-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016645.
XX
PR   24-MAY-2002; 2002US-0383212P.
XX
PA   (REST-) RESTORAGEN INC.
XX
PI   Xia Y,  Peng L;
XX
DR   WPI; 2004-035129/03.
DR   P-PSDB; ADJ65838.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 34; 132pp; English.
XX
CC   The invention comprises an expression cassette which produces a tandem
CC   polypeptide that form an inclusion body when expressed in a cell. The
CC   expression cassette of the invention is useful for producing a peptide or
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present DNA sequence encodes
CC   a peptide which may be used in the construction of a tandem polypeptide
CC   of the invention.
XX
SQ   Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;

  Query Match             74.8%;  Score 69.6;  DB 12;  Length 111;
  Best Local Similarity   63.0%;  Pred. No. 1.9e-14;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 10
ADW14375
ID   ADW14375 standard; DNA; 111 BP.
XX
AC   ADW14375;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human parathyroxin Gly-Ser-Pro-PTH 1-34 peptide DNA SEQ ID NO:1.
XX
KW   ds; parathyroxin; recombinant protein; protein engineering.
XX
OS   Homo sapiens.
XX
PN   CN1424325-A.
XX
PD   18-JUN-2003.
XX
PF   12-DEC-2001; 2001CN-00142627.
XX
PR   12-DEC-2001; 2001CN-00142627.
XX
PA   (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.
XX
```

PI Chen C, Xiu C, Li M;
XX
DR WPI; 2004-099606/11.
DR P-PSDB; ADW14376.
XX
PT Production of reorganized human parathyroid hormone 1-34 peptide.
XX
PS Claim 3; SEQ ID NO 1; 25pp; Chinese.
XX
CC The invention relates to a novel process for preparing recombinant human
CC parathyroxin 1-34 peptide, including such steps as culturing a host cell
CC in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376),
CC severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and
CC separating and purifying PTH 1-34 peptide. The present sequence encodes
CC the Gly-Ser-Pro-PTH 1-34 peptide.
XX
SQ Sequence 111 BP; 31 A; 28 C; 25 G; 27 T; 0 U; 0 Other;

Query Match 74.8%; Score 69.6; DB 13; Length 111;
Best Local Similarity 63.0%; Pred. No. 1.9e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

Qy 2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
Db 11 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 70

Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
Db 71 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 102

RESULT 11
ADG93260
ID ADG93260 standard; DNA; 117 BP.
XX
AC ADG93260;
XX
DT 11-MAR-2004 (first entry)
XX
DE Novel expression cassette-related PTH DNA SeqID141.
XX
KW expression cassette; high yield polypeptide production;
KW tandem polypeptide; inclusion body; gene; ds; PTH.
XX
OS Unidentified.
OS Synthetic.
XX
PN WO2003100021-A2.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-US016643.
XX
PR 24-MAY-2002; 2002US-0383370P.
XX
PA (REST-) RESTORAGEN INC.
PA (HARL/) HARLEY S.
XX
PI Harley S, Williams JA, Luan P, Xia Y;
XX
DR WPI; 2004-035128/03.
DR P-PSDB; ADG93259.
XX
PT New expression cassette comprising an operably linked nucleic acid
PT sequence, useful for producing a tandem polypeptide that forms an
PT inclusion body when expressed in a cell.
XX
PS Disclosure; SEQ ID NO 141; 157pp; English.
XX
CC This invention relates to a novel expression cassette and methods for
CC high yield production of polypeptides. The cassette comprises an operably
CC linked nucleic acid sequence, where the expression of the cassette
CC produces a tandem polypeptide that forms an inclusion body when expressed
CC in a cell. The expression cassette is useful for producing peptide and
CC polypeptide in a cell, preferably a tandem polypeptide that forms an
CC inclusion body when expressed in a cell. The present sequence is that of
CC a DNA sequence which encodes a PTH peptide which was used in the
CC exemplification of the invention.
XX
SQ Sequence 117 BP; 35 A; 27 C; 25 G; 30 T; 0 U; 0 Other;

Query Match 74.8%; Score 69.6; DB 12; Length 117;
Best Local Similarity 63.0%; Pred. No. 1.9e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

Qy 2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
Db 2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
Db 62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93

RESULT 12
AAT34865
ID AAT34865 standard; cDNA; 168 BP.
XX
AC AAT34865;
XX
DT 02-DEC-1996 (first entry)
XX
DE Plasmid pBN1:PTH(1-34)C-1c portion encoding PTH(1-34)Cys.
XX
KW PTH; parathyroid hormone; parathormone; C-amide; C-amidated peptide;
KW alpha-carboxamide; recombinant protein; fusion protein; transpeptidation;
KW vector; plasmid pBN1; carbonic anhydrase II; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .162
FT /*tag= a
FT /product= "hCA-linker-PTH(1-34)Cys fusion"
XX
PN WO9617941-A2.
XX
PD 13-JUN-1996.
XX
PF 07-DEC-1995; 95WO-US015799.
XX
PR 07-DEC-1994; 94US-00350528.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Stout JS, Patridge BE, Heriksen DB, Holmquist B, Wagner FW;
XX
DR WPI; 1996-287185/29.
DR P-PSDB; AAR98967.
XX
PT Production of C-terminal alpha-carboxamidated peptide(s) - by cleavage
PT and transpeptidation of recombinant multicopy peptide(s) or fusion
PT constructs.
XX
PS Example 7; Fig 1; 93pp; English.
XX
CC A portion (AAT34865) of plasmid pBN1:PTH(1-34)C-1c comprises DNA coding
CC for a fusion protein (AAR87867) composed of the C-terminal end of human
CC carbonic anhydrase II joined by an intraconnecting peptide (including a
CC thrombin cleavage site) to amino acids 1-34 of PTH (AAR98966), followed
CC by a Cys residue and C-terminal sequence. The complete construct can be
CC expressed in E. coli transformants. The intraconnecting peptide and C-
CC terminal Cys residue enable the recombinant protein construct to be
CC selectively reacted to produce C-terminal carboxamidated PTH(1-34)
XX
SQ Sequence 168 BP; 41 A; 44 C; 42 G; 41 T; 0 U; 0 Other;

```
  Query Match             74.8%;  Score 69.6;  DB 2;  Length 168;
  Best Local Similarity   63.0%;  Pred. No. 2.1e-14;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:||||||:|
Db         47 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 106

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        107 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 138


RESULT 13
ADG93181
ID   ADG93181 standard; DNA; 252 BP.
XX
AC   ADG93181;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel expression cassette-related polypeptide-encoding DNA SeqID62.
XX
KW   expression cassette; high yield polypeptide production;
KW   tandem polypeptide; inclusion body; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100021-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016643.
XX
PR   24-MAY-2002; 2002US-0383370P.
XX
PA   (REST-) RESTORAGEN INC.
PA   (HARL/) HARLEY S.
XX
PI   Harley S,  Williams JA,  Luan P,  Xia Y;
XX
DR   WPI; 2004-035128/03.
DR   P-PSDB; ADG93161.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 62; 157pp; English.
XX
CC   This invention relates to a novel expression cassette and methods for
CC   high yield production of polypeptides. The cassette comprises an operably
CC   linked nucleic acid sequence, where the expression of the cassette
CC   produces a tandem polypeptide that forms an inclusion body when expressed
CC   in a cell. The expression cassette is useful for producing peptide and
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present sequence is that of
CC   a DNA sequence which encodes a polypeptide which may be produced using
CC   the expression cassette of the invention.
XX
SQ   Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;

  Query Match             74.8%;  Score 69.6;  DB 12;  Length 252;
  Best Local Similarity   63.0%;  Pred. No. 2.4e-14;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
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Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 14
ADJ65859
ID   ADJ65859 standard; DNA; 252 BP.
XX
AC   ADJ65859;
XX
DT   06-MAY-2004  (first entry)
XX
DE   PTH protein coding sequence.
XX
KW   expression cassette; tandem polypeptide; inclusion body;
KW   inclusion body fusion partner; PTH; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100022-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016645.
XX
PR   24-MAY-2002; 2002US-0383212P.
XX
PA   (REST-) RESTORAGEN INC.
XX
PI   Xia Y,  Peng L;
XX
DR   WPI; 2004-035129/03.
DR   P-PSDB; ADJ65839.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 35; 132pp; English.
XX
CC   The invention comprises an expression cassette which produces a tandem
CC   polypeptide that form an inclusion body when expressed in a cell. The
CC   expression cassette of the invention is useful for producing a peptide or
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present DNA sequence encodes
CC   a protein which may be used in the construction of a tandem polypeptide
CC   of the invention.
XX
SQ   Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;

  Query Match             74.8%;  Score 69.6;  DB 12;  Length 252;
  Best Local Similarity   63.0%;  Pred. No. 2.4e-14;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 15
ADJ65913
ID   ADJ65913 standard; DNA; 264 BP.
XX
AC   ADJ65913;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Tandem polypeptide-encoding expression cassette #6.
XX
KW   expression cassette; tandem polypeptide; inclusion body;
```

KW inclusion body fusion partner; gene; ds.
XX
OS Unidentified.
XX
PN WO2003100022-A2.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-US016645.
XX
PR 24-MAY-2002; 2002US-0383212P.
XX
PA (REST-) RESTORAGEN INC.
XX
PI Xia Y, Peng L;
XX
DR WPI; 2004-035129/03.
DR P-PSDB; ADJ65912.
XX
PT New expression cassette comprising an operably linked nucleic acid
PT sequence, useful for producing a tandem polypeptide that forms an
PT inclusion body when expressed in a cell.
XX
PS Disclosure; SEQ ID NO 89; 132pp; English.
XX
CC The invention comprises an expression cassette which produces a tandem
CC polypeptide that form an inclusion body when expressed in a cell. The
CC expression cassette of the invention is useful for producing a peptide or
CC polypeptide in a cell, preferably a tandem polypeptide that forms an
CC inclusion body when expressed in a cell. The present DNA sequence
CC represents an expression cassette which encodes a tandem polypeptide of
CC the invention.
XX
SQ Sequence 264 BP; 72 A; 67 C; 64 G; 61 T; 0 U; 0 Other;

Query Match 74.8%; Score 69.6; DB 12; Length 264;
Best Local Similarity 63.0%; Pred. No. 2.4e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:|||       ||:      |:||||:| |:|||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:||||||||:||||||||::
Db         65 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 96
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Search completed: November 23, 2005, 23:00:14
Job time : 244.667 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:35:17 ; Search time 1177.67 Seconds
(without alignments)
4488.911 Million cell updates/sec

Title: US-09-475-158A-14
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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10: gb_sts:*
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12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	93	100.0	93	6	BD266832	BD266832 PTH funct
	2	83.4	89.7	93	6	BD266833	BD266833 PTH funct
	3	73.8	79.4	93	6	BD266834	BD266834 PTH funct
	4	66.4	71.4	258	6	AR269042	AR269042 Sequence
	5	63.8	68.6	141	6	AR005132	AR005132 Sequence
c	6	63.8	68.6	141	6	AR005133	AR005133 Sequence
	7	63.8	68.6	141	6	AR177779	AR177779 Sequence
c	8	63.8	68.6	141	6	AR177780	AR177780 Sequence
	9	63.8	68.6	207	6	AR043797	AR043797 Sequence
	10	60	64.5	405	6	BD234383	BD234383 Recombina
	11	60	64.5	408	6	BD234385	BD234385 Recombina
	12	60	64.5	408	6	BD234386	BD234386 Recombina
	13	60	64.5	411	6	BD234384	BD234384 Recombina
	14	60	64.5	414	6	BD234390	BD234390 Recombina
	15	60	64.5	417	6	BD234387	BD234387 Recombina
	16	60	64.5	423	6	BD234388	BD234388 Recombina
	17	60	64.5	435	6	BD234389	BD234389 Recombina
	18	57.4	61.7	717	6	A36847	A36847 Sequence 1
	19	57.4	61.7	945	6	A36849	A36849 Sequence 3
	20	54.2	58.3	252	6	AR027046	AR027046 Sequence
	21	54.2	58.3	252	6	E05675	E05675 DNA encodin
	22	52.6	56.6	252	6	AR027011	AR027011 Sequence
	23	52.6	56.6	252	6	AR027044	AR027044 Sequence
	24	52.6	56.6	252	6	AR030635	AR030635 Sequence
	25	52.6	56.6	252	6	AR168173	AR168173 Sequence
	26	52.6	56.6	252	6	E05658	E05658 DNA encodin
	27	52.6	56.6	252	6	E05673	E05673 DNA encodin
	28	52.6	56.6	252	6	I83594	I83594 Sequence 1
	29	52.6	56.6	263	6	AR027020	AR027020 Sequence
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	31	52.6	56.6	263	6	E05671	E05671 DNA encodin
	32	52.6	56.6	263	6	I83595	I83595 Sequence 3
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c	34	52.6	56.6	265	6	AR027021	AR027021 Sequence
c	35	52.6	56.6	265	6	E05672	E05672 DNA encodin
c	36	52.6	56.6	265	6	I83596	I83596 Sequence 4
	37	51	54.8	102	6	BD170195	BD170195 Process f
	38	51	54.8	186	6	BD170222	BD170222 Process f
	39	51	54.8	201	6	BD170213	BD170213 Process f
	40	51	54.8	225	6	BD170211	BD170211 Process f
	41	51	54.8	240	6	BD170198	BD170198 Process f
	42	51	54.8	252	6	AR027050	AR027050 Sequence
	43	51	54.8	252	6	BD170196	BD170196 Process f
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ALIGNMENTS

RESULT 1
BD266832
LOCUS BD266832 93 bp RNA linear PAT 17-JUL-2003
DEFINITION PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.
ACCESSION BD266832
VERSION BD266832.1 GI:33076600
KEYWORDS JP 2002533115-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 93)
AUTHORS Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
TITLE PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules
JOURNAL Patent: JP 2002533115-A 1 08-OCT-2002;
THE GENERAL HOSPITAL CORP
COMMENT OS Artificial Sequence
PN JP 2002533115-A/1
PD 08-OCT-2002
PF 30-DEC-1999 JP 2000591171
PR 31-DEC-1998 US 60/114577
PI THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD PI JUEPPNER
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC A61P19/10,
PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: modified PTH sequence FH Key Location/Qualifiers
FT source 1. .93
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .93
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ORIGIN

Query Match 100.0%; Score 93; DB 6; Length 93;

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  Best Local Similarity   74.2%;  Pred. No. 1.4e-20;
  Matches   69;  Conservative   24;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||:|:::||||||:|||||:||:||||||:||:||:||:|:|||||:|||:||||||:
Db          1 GCTGTTTCCGAAATCCAGCTGATGCACGGTGGTGGTGGTGGTCTGAACTCCATGGAACGT 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |::|||:|||:|||:|||||||:||||||::
Db         61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 2
BD266833
LOCUS       BD266833                 93 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules.
ACCESSION   BD266833
VERSION     BD266833.1  GI:33076601
KEYWORDS    JP 2002533115-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
  TITLE     PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules
  JOURNAL   Patent: JP 2002533115-A 2 08-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002533115-A/2
            PD   08-OCT-2002
            PF   30-DEC-1999 JP 2000591171
            PR   31-DEC-1998 US    60/114577
            PI   THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD  PI
            JUEPPNER
            PC   C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC
              A61P19/10,
            PC   A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
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ORIGIN

  Query Match             89.7%;  Score 83.4;  DB 6;  Length 93;
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  Matches   64;  Conservative   23;  Mismatches    6;  Indels    0;  Gaps    0;

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              ||:|:::||||||:|||||:||:||||||:||:||:||:||:      :|||:||||||:
Db          1 GCTGTTTCCGAAATCCAGCTGATGCACGGTGGTGGTGGTGGTGGTTCCATGGAACGT 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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Db         61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 3
BD266834
LOCUS       BD266834                 93 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules.
ACCESSION   BD266834
VERSION     BD266834.1  GI:33076602
KEYWORDS    JP 2002533115-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
  TITLE     PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules
  JOURNAL   Patent: JP 2002533115-A 3 08-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002533115-A/3
            PD   08-OCT-2002
            PF   30-DEC-1999 JP 2000591171
            PR   31-DEC-1998 US    60/114577
            PI   THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD  PI
            JUEPPNER
            PC   C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC
              A61P19/10,
            PC   A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
            Description of Artificial Sequence: modified PTH sequence FH   Key
                     Location/Qualifiers
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ORIGIN

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  Matches   59;  Conservative   22;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||:|:::||||||:|             ||:||:||:||:||:|:||||:|||:|||||:
Db          1 GCTGTTTCCGAAATCGGTGGTGGTGGTGGTGGTGGTGGTCTGAACTCCATGGAACGT 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |::|||:|||:|||:|||||||:||||||::
Db         61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 4
AR269042
LOCUS       AR269042                 258 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6500647.
ACCESSION   AR269042
VERSION     AR269042.1  GI:29699873
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 258)
  AUTHORS   Jung,E.-K., Park,D.-H. and Chung,S.-I.
  TITLE     Recombinant expression vector of human parathyroid hormone
  JOURNAL   Patent: US 6500647-A 26 31-DEC-2002;
            Mogam Biotechnology Research Institute; Kyonggi-Do;
            KRX;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             71.4%;  Score 66.4;  DB 6;  Length 258;
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  Matches   55;  Conservative   21;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||: |:|||       ||:     :|:|||||:| |:|||||:|
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```
Db          2 CTGTTTCGGAAATCCAGCTTATGCATAACCTGGGTAAACATCTGAACTCGATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
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Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGATGTT 93


RESULT 5
AR005132
LOCUS       AR005132                 141 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5747453.
ACCESSION   AR005132
VERSION     AR005132.1  GI:3966011
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 5747453-A 3 05-MAY-1998;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           68.6%;  Score 63.8;  DB 6;  Length 141;
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  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:      |:||||:|| : || ||:|
Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||:
Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 6
AR005133/c
LOCUS       AR005133                 141 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5747453.
ACCESSION   AR005133
VERSION     AR005133.1  GI:3966012
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 5747453-A 5 05-MAY-1998;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           68.6%;  Score 63.8;  DB 6;  Length 141;
  Best Local Similarity   61.5%;  Pred. No. 1.2e-10;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:      |:||||:|| : || ||:|
Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 7
AR177779
LOCUS       AR177779                 141 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 3 from patent US 6313092.
ACCESSION   AR177779
VERSION     AR177779.1  GI:17920134
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 6313092-A 3 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .141
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ORIGIN

  Query Match           68.6%;  Score 63.8;  DB 6;  Length 141;
  Best Local Similarity   61.5%;  Pred. No. 1.2e-10;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:      |:||||:|| : || ||:|
Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||:
Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 8
AR177780/c
LOCUS       AR177780                 141 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 5 from patent US 6313092.
ACCESSION   AR177780
VERSION     AR177780.1  GI:17920135
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 6313092-A 5 06-NOV-2001;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

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  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

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Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
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Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 9
AR043797
LOCUS       AR043797                 207 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5814603.
ACCESSION   AR043797
VERSION     AR043797.1  GI:5964805
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 207)
  AUTHORS   Oldenburg,K.R. and Selick,H.E.
  TITLE     Compounds with PTH activity
  JOURNAL   Patent: US 5814603-A 8 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .207
                     /organism="unknown"
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ORIGIN

  Query Match             68.6%;  Score 63.8;  DB 6;  Length 207;
  Best Local Similarity   61.5%;  Pred. No. 1.2e-10;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:      |:||||:|| : || ||:|
Db         71 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 130

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
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Db        131 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 161


RESULT 10
BD234383
LOCUS       BD234383                405 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234383
VERSION     BD234383.1  GI:33044153
KEYWORDS    JP 2002533072-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 4 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/4
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: PCpB-RVR-hPTH fusion FH
            Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

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              |:|:::| ||||:|||||:||:|||       ||      :|:||||:| |:||| ||:|
Db        293 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 352

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RESULT 11
BD234385
LOCUS       BD234385                408 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234385
VERSION     BD234385.1  GI:33044155
KEYWORDS    JP 2002533072-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 6 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/6
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
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            Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
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Db        296 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 355

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              : |||:|||:|||:|| || |:|||||| |::
Db        356 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 387


RESULT 12
BD234386
LOCUS       BD234386                408 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234386
VERSION     BD234386.1  GI:33044156
KEYWORDS    JP 2002533072-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 7 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/7
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
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ORIGIN

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  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
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Db        296 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 355

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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Db        356 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 387


RESULT 13
BD234384
LOCUS       BD234384                411 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234384
VERSION     BD234384.1  GI:33044154
KEYWORDS    JP 2002533072-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 5 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/5
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
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            Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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Db        359 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 390


RESULT 14
BD234390
LOCUS       BD234390                414 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234390
VERSION     BD234390.1  GI:33044160
KEYWORDS    JP 2002533072-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 11 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/11
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: PCpB-APR-hPTH fusion FH
            Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
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Db        302 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 361

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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RESULT 15
BD234387
LOCUS       BD234387                417 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234387
VERSION     BD234387.1  GI:33044157
KEYWORDS    JP 2002533072-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 417)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 8 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/8
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: PCpB-VIPR-hPTH fusion FH
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FEATURES             Location/Qualifiers
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ORIGIN

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Db         305 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 364

Qy          62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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GenCore version 5.1.6

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Total number of hits satisfying chosen parameters: 82156650

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	47.8	51.4	416	8	W31998	W31998 zb96d06.r1
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ALIGNMENTS

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DEFINITION zb39c01.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305952 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W19763
VERSION W19763.1 GI:1295880
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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High quality sequence stop: 222.
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/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 52.0%; Score 48.4; DB 8; Length 324;
Best Local Similarity 53.8%; Pred. No. 2.9e-05;
Matches 49; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :|:||||:| |:|||  | |
Db         60 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 119

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        120 TAGAATGGCTGCGTAAGAANCTGCAGGATGT 150
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RESULT 2
W39062
LOCUS W39062 352 bp mRNA linear EST 15-MAY-1996
DEFINITION zb34c06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305482 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W39062
VERSION W39062.1 GI:1320771
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 352)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 286.

FEATURES Location/Qualifiers
source 1. .352
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248892"
/db_xref="taxon:9606"
/clone="IMAGE:305482"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 51.4%; Score 47.8; DB 8; Length 352;
Best Local Similarity 53.8%; Pred. No. 4.7e-05;
Matches 49; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :|:||||:| |:|||  | |
Db        185 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 244

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        245 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 275
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RESULT 3
W38966
LOCUS W38966 376 bp mRNA linear EST 15-MAY-1996
DEFINITION zb28b12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304895 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W38966
VERSION W38966.1 GI:1320674
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 376)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET.

FEATURES Location/Qualifiers
source 1. .376
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248305"
/db_xref="taxon:9606"
/clone="IMAGE:304895"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT

TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 51.4%; Score 47.8; DB 8; Length 376;
Best Local Similarity 53.8%; Pred. No. 4.7e-05;
Matches 49; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :|:||||:| |:|||  | |
Db        172 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 231

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        232 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 262
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RESULT 4
W37708
LOCUS W37708 411 bp mRNA linear EST 10-OCT-1996
DEFINITION zc10d12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321911 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W37708
VERSION W37708.1 GI:1319302
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 876 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 396.
FEATURES Location/Qualifiers
source 1. .411
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1259569"
/db_xref="taxon:9606"
/clone="IMAGE:321911"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTT

TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 51.4%; Score 47.8; DB 8; Length 411;
Best Local Similarity 53.8%; Pred. No. 4.8e-05;
Matches 49; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :|:||||:| |:|||  | |
Db        210 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 269

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        270 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 300
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RESULT 5
W31998
LOCUS W31998 416 bp mRNA linear EST 20-AUG-1996
DEFINITION zb96d06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:320651 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W31998
VERSION W31998.1 GI:1313010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 416)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 771 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 386.
FEATURES Location/Qualifiers
source 1. .416
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258309"
/db_xref="taxon:9606"
/clone="IMAGE:320651"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

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  Query Match             51.4%;  Score 47.8;  DB 8;  Length 416;
  Best Local Similarity   53.8%;  Pred. No. 4.8e-05;
  Matches   49;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :|:||||:| |:|||  | |
Db         34 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 93

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db         94 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 124
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RESULT 6
W38764
LOCUS W38764 434 bp mRNA linear EST 15-MAY-1996
DEFINITION zb27a07.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304788 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W38764
VERSION W38764.1 GI:1320471
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 253.

FEATURES Location/Qualifiers
source 1. .434
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248198"
/db_xref="taxon:9606"
/clone="IMAGE:304788"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer {5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

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  Query Match             51.4%;  Score 47.8;  DB 8;  Length 434;
  Best Local Similarity   53.8%;  Pred. No. 4.8e-05;
  Matches   49;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :|:||||:| |:|||  | |
Db        174 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 233

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        234 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 264
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RESULT 7
W56235
LOCUS W56235 450 bp mRNA linear EST 10-OCT-1996
DEFINITION zc01e11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321068 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W56235
VERSION W56235.1 GI:1358124
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 450)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 865 Std Error: 0.00
Seq primer: mob.REGA+ET.

FEATURES Location/Qualifiers
source 1. .450
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258726"
/db_xref="taxon:9606"
/clone="IMAGE:321068"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 51.4%; Score 47.8; DB 8; Length 450;
Best Local Similarity 53.8%; Pred. No. 4.9e-05;
Matches 49; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :|:||||:| |:|||  | |
Db        189 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 248

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        249 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 279
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RESULT 8
W33077
LOCUS W33077 453 bp mRNA linear EST 10-OCT-1996
DEFINITION zc07a12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321598 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W33077
VERSION W33077.1 GI:1315062
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 453)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 871 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 367.

FEATURES Location/Qualifiers
source 1. .453
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1259256"
/db_xref="taxon:9606"
/clone="IMAGE:321598"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 51.4%; Score 47.8; DB 8; Length 453;
Best Local Similarity 53.8%; Pred. No. 4.9e-05;
Matches 49; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :|:||||:| |:|||  | |
Db        201 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 260

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        261 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 291
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RESULT 9
W56820
LOCUS W56820 496 bp mRNA linear EST 10-OCT-1996
DEFINITION zc01a03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321004 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W56820
VERSION W56820.1 GI:1358743
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 496)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 858 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 424.

FEATURES Location/Qualifiers
source 1. .496
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258662"
/db_xref="taxon:9606"
/clone="IMAGE:321004"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             51.4%;  Score 47.8;  DB 8;  Length 496;
  Best Local Similarity   53.8%;  Pred. No. 5e-05;
  Matches   49;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :|:||||:| |:|||  | |
Db        179 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 238

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        239 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 269
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RESULT 10
W19765
LOCUS W19765 536 bp mRNA linear EST 03-MAY-1996
DEFINITION zb39c03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305956 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W19765
VERSION W19765.1 GI:1295882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 536)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 352.
FEATURES Location/Qualifiers
source 1. .536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249366"
/db_xref="taxon:9606"
/clone="IMAGE:305956"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             51.4%;  Score 47.8;  DB 8;  Length 536;
  Best Local Similarity   53.8%;  Pred. No. 5e-05;
  Matches   49;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :|:||||:| |:|||  | |
Db        189 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 248

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        249 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 279
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RESULT 11
W56120
LOCUS W56120 576 bp mRNA linear EST 11-OCT-1996
DEFINITION zc56h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326363 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W56120
VERSION W56120.1 GI:1358009
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 576)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 904 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 433.
FEATURES Location/Qualifiers
source 1. .576
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1260565"
/db_xref="taxon:9606"
/clone="IMAGE:326363"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT

TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             51.4%;  Score 47.8;  DB 8;  Length 576;
  Best Local Similarity   53.8%;  Pred. No. 5.1e-05;
  Matches   49;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :|:||||:| |:|||  | |
Db        184 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 243

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        244 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 274
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RESULT 12
W39202
LOCUS W39202 583 bp mRNA linear EST 15-MAY-1996
DEFINITION zb35h03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305621 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W39202
VERSION W39202.1 GI:1320911
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 400.

FEATURES Location/Qualifiers
source 1. .583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249031"
/db_xref="taxon:9606"
/clone="IMAGE:305621"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             51.4%;  Score 47.8;  DB 8;  Length 583;
  Best Local Similarity   53.8%;  Pred. No. 5.1e-05;
  Matches   49;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :|:||||:| |:|||  | |
Db         53 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 112

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        113 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 143
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RESULT 13
BG198564
LOCUS BG198564 721 bp mRNA linear EST 21-APR-2001
DEFINITION RST17829 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG198564
VERSION BG198564.1 GI:13720251
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 721)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 549.

FEATURES Location/Qualifiers
source 1. .721
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

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  Query Match             51.4%;  Score 47.8;  DB 2;  Length 721;
  Best Local Similarity   53.8%;  Pred. No. 5.3e-05;
  Matches   49;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :|:||||:| |:|||  | |
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```
Db        112 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 171

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        172 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 202


RESULT 14
AI051997/c
LOCUS       AI051997                741 bp    mRNA    linear   EST 10-JUL-1998
DEFINITION  oy29c05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:1667240 3' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   AI051997
VERSION     AI051997.1  GI:3307988
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 444.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1667240"
                     /tissue_type="parathyroid tumor"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_parathyroid_tumor_NbHPA"
                     /note="Organ: parathyroid gland; Vector: pT7T3D
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT
                     TTTTT-3'], double-stranded cDNA was size selected, ligated
                     to Eco RI adapters (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of a modified pT7T3
                     vector (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                     adenomas was kindly provided by Dr. Stephen Marx, National
                     Institute of Diabetes and Digestive and Kidney Diseases,
                     NIH."
ORIGIN

  Query Match             51.4%;  Score 47.8;  DB 1;  Length 741;
  Best Local Similarity   53.8%;  Pred. No. 5.3e-05;
  Matches   49;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :|:||||:| |:|||  | |
Db        618 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 559

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
```

```
Db        558 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 528


RESULT 15
BX106232
LOCUS       BX106232                757 bp    mRNA    linear   EST 06-FEB-2003
DEFINITION  BX106232 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGp998J24728 ; IMAGE:321911, mRNA sequence.
ACCESSION   BX106232
VERSION     BX106232.1  GI:27846872
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998J24728.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .757
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998J24728 ; IMAGE:321911"
                     /tissue_type="parathyroid tumor"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_parathyroid_tumor_NbHPA"
                     /note="Organ: parathyroid gland; Vector: pT7T3D
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT
                     TTTTT-3'], double-stranded cDNA was size selected, ligated
                     to Eco RI adapters (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of a modified pT7T3
                     vector (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                     adenomas was kindly provided by Dr. Stephen Marx, National
                     Institute of Diabetes and Digestive and Kidney Diseases,
                     NIH."
ORIGIN

  Query Match             51.4%;  Score 47.8;  DB 5;  Length 757;
  Best Local Similarity   53.8%;  Pred. No. 5.3e-05;
  Matches   49;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :|:||||:| |:|||  | |
Db        210 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 269

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
```

Db 270 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 300

Search completed: November 24, 2005, 01:30:28
Job time : 1825 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:44:43 ; Search time 73.6667 Seconds
(without alignments)
2244.071 Million cell updates/sec

Title: US-09-475-158A-14
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	66.4	71.4	258	3	US-09-463-282D-26	Sequence 26, Appl
	2	63.8	68.6	141	2	US-08-468-275-3	Sequence 3, Appli
c	3	63.8	68.6	141	2	US-08-468-275-5	Sequence 5, Appli
	4	63.8	68.6	141	3	US-09-007-466-3	Sequence 3, Appli
c	5	63.8	68.6	141	3	US-09-007-466-5	Sequence 5, Appli
	6	63.8	68.6	141	3	US-08-952-980B-3	Sequence 3, Appli
c	7	63.8	68.6	141	3	US-08-952-980B-5	Sequence 5, Appli
	8	63.8	68.6	207	2	US-08-142-551B-8	Sequence 8, Appli
	9	54.2	58.3	252	2	US-08-733-446-58	Sequence 58, Appl
	10	52.6	56.6	102	3	US-10-340-484-14	Sequence 14, Appl
	11	52.6	56.6	252	2	US-08-689-190-1	Sequence 1, Appli
	12	52.6	56.6	252	2	US-08-733-446-23	Sequence 23, Appl
	13	52.6	56.6	252	2	US-08-733-446-56	Sequence 56, Appl
	14	52.6	56.6	252	2	US-08-835-231-34	Sequence 34, Appl
	15	52.6	56.6	252	3	US-09-108-661-34	Sequence 34, Appl
	16	52.6	56.6	263	2	US-08-689-190-3	Sequence 3, Appli
	17	52.6	56.6	263	2	US-08-733-446-32	Sequence 32, Appl
c	18	52.6	56.6	265	2	US-08-689-190-4	Sequence 4, Appli
c	19	52.6	56.6	265	2	US-08-733-446-33	Sequence 33, Appl
	20	51	54.8	252	2	US-08-733-446-62	Sequence 62, Appl
	21	49.4	53.1	252	2	US-08-733-446-57	Sequence 57, Appl
c	22	48.4	52.0	74	2	US-08-142-551B-132	Sequence 132, App
	23	47.8	51.4	252	2	US-07-863-014-1	Sequence 1, Appli
	24	47.8	51.4	252	2	US-08-332-453-1	Sequence 1, Appli
	25	47.8	51.4	537	2	US-08-835-231-5	Sequence 5, Appli
	26	47.8	51.4	537	2	US-08-835-231-6	Sequence 6, Appli
	27	47.8	51.4	537	3	US-09-108-661-5	Sequence 5, Appli
	28	47.8	51.4	537	3	US-09-108-661-6	Sequence 6, Appli
c	29	47.8	51.4	601	3	US-09-949-016-18519	Sequence 18519, A
c	30	47.8	51.4	601	3	US-09-949-016-66782	Sequence 66782, A
	31	47.8	51.4	772	3	US-09-949-016-51	Sequence 51, Appl
	32	47.8	51.4	773	3	US-09-949-016-1970	Sequence 1970, Ap
	33	47.8	51.4	7926	3	US-09-949-016-11793	Sequence 11793, A
	34	47.8	51.4	7926	3	US-09-949-016-13712	Sequence 13712, A
	35	46.2	49.7	243	2	US-08-733-446-22	Sequence 22, Appl
	36	46.2	49.7	254	2	US-08-733-446-30	Sequence 30, Appl
c	37	46.2	49.7	256	2	US-08-733-446-31	Sequence 31, Appl
	38	44.8	48.2	240	2	US-08-733-446-21	Sequence 21, Appl
	39	44.8	48.2	248	2	US-08-733-446-26	Sequence 26, Appl
	40	44.8	48.2	251	2	US-08-733-446-28	Sequence 28, Appl
c	41	44.8	48.2	253	2	US-08-733-446-29	Sequence 29, Appl
c	42	43.8	47.1	250	2	US-08-733-446-27	Sequence 27, Appl
	43	43.4	46.7	45	3	US-09-463-282D-5	Sequence 5, Appli
	44	43.4	46.7	237	2	US-08-733-446-20	Sequence 20, Appl
	45	43	46.2	67	3	US-09-068-738A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-463-282D-26
; Sequence 26, Application US/09463282D
; Patent No. 6500647
; GENERAL INFORMATION:
; APPLICANT: Jung, Eun-Kyung
; APPLICANT: Park, Doo-Hong
; APPLICANT: Chung, Soo Il
; TITLE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE
; FILE REFERENCE: 0136/0G626
; CURRENT APPLICATION NUMBER: US/09/463,282D
; CURRENT FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: PCT/KR98/00146
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: KR 1997-35230
; PRIOR FILING DATE: 1997-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-463-282D-26

Query Match 71.4%; Score 66.4; DB 3; Length 258;
Best Local Similarity 59.8%; Pred. No. 2.5e-13;
Matches 55; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

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Db          2 CTGTTTCGGAAATCCAGCTTATGCATAACCTGGGTAAACATCTGAACTCGATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
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Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGATGTT 93
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RESULT 2
US-08-468-275-3
; Sequence 3, Application US/08468275
; Patent No. 5747453
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 10

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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,275
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..138
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  25
US-08-468-275-3

  Query Match             68.6%;  Score 63.8;  DB 2;  Length 141;
  Best Local Similarity   61.5%;  Pred. No. 1.7e-12;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
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Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 3
US-08-468-275-5/c
; Sequence 5, Application US/08468275
; Patent No. 5747453
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,275
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-468-275-5

  Query Match             68.6%;  Score 63.8;  DB 2;  Length 141;
  Best Local Similarity   61.5%;  Pred. No. 1.7e-12;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:      |:||||:|| : || ||:|
Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 4
US-09-007-466-3
; Sequence 3, Application US/09007466
; Patent No. 6313092
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/007,466
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/468,275
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..138
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  25
US-09-007-466-3

  Query Match             68.6%;  Score 63.8;  DB 3;  Length 141;
  Best Local Similarity   61.5%;  Pred. No. 1.7e-12;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::|||||||:|||||:| :||||      ||:      |:||||:|| : || ||:|
Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:||||||||:||||||||:
Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 5
US-09-007-466-5/c
; Sequence 5, Application US/09007466
; Patent No. 6313092
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/007,466
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/468,275
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-007-466-5

  Query Match             68.6%;  Score 63.8;  DB 3;  Length 141;
  Best Local Similarity   61.5%;  Pred. No. 1.7e-12;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
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Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:||||||||:||||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 6
US-08-952-980B-3
; Sequence 3, Application US/08952980B
; Patent No. 6333189
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/952,980B
;      FILING DATE:  20-NOV-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  2349 CIP 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 496-8150
;      TELEFAX:  (650) 496-8048
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..138
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  25
US-08-952-980B-3

  Query Match             68.6%;  Score 63.8;  DB 3;  Length 141;
  Best Local Similarity   61.5%;  Pred. No. 1.7e-12;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
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Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

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              ::|||:|||:|||:||||||||:||||||||:
Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 7
US-08-952-980B-5/c
; Sequence 5, Application US/08952980B
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; Patent No. 6333189
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/952,980B
;      FILING DATE:  20-NOV-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  2349 CIP 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 496-8150
;      TELEFAX:  (650) 496-8048
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-952-980B-5

  Query Match             68.6%;  Score 63.8;  DB 3;  Length 141;
  Best Local Similarity   61.5%;  Pred. No. 1.7e-12;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

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Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

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Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 8
US-08-142-551B-8
; Sequence 8, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  207 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..201
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..51
;      OTHER INFORMATION:  /note= "Encodes the leader peptide
;      OTHER INFORMATION:  sequence that serves to direct the protein into
;      OTHER INFORMATION:  inclusion bodies."
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  70..174
;      OTHER INFORMATION:  /note= "Encodes the protein or
;      OTHER INFORMATION:  peptide of interest"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  175..207
;      OTHER INFORMATION:  /note= "Encodes amino acid sequence
;      OTHER INFORMATION:  having six histamines that serves as a tag for the
;      OTHER INFORMATION:  purification of the protein on a nickel column."
US-08-142-551B-8

  Query Match             68.6%;  Score 63.8;  DB 2;  Length 207;
  Best Local Similarity   61.5%;  Pred. No. 1.9e-12;
  Matches   56;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:      |:||||:|| : || ||:|
Db         71 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 130

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db        131 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 161


RESULT 9
US-08-733-446-58
; Sequence 58, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..252
;      NAME/KEY:  mutation
;      LOCATION:  19...24
;      IDENTIFICATION METHOD:  E
US-08-733-446-58

  Query Match             58.3%;  Score 54.2;  DB 2;  Length 252;
  Best Local Similarity   54.9%;  Pred. No. 4e-09;
  Matches   50;  Conservative   18;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|: :|||| |: ||||:| :|||      :||      : :||||:|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGCTGCTGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 10
US-10-340-484-14
; Sequence 14, Application US/10340484
; Patent No. 6875739
; GENERAL INFORMATION:
;  APPLICANT: Stewart, Andrew F.
;  TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
;  TITLE OF INVENTION:  Drugs
;  FILE REFERENCE: 25200-501
;  CURRENT APPLICATION NUMBER: US/10/340,484
;  CURRENT FILING DATE:  2003-01-10
;  PRIOR APPLICATION NUMBER: 60/347,215
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: 60/353,296
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: 60/368,955
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: 60/379,125
;  PRIOR FILING DATE: 2002-05-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 102
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-340-484-14

  Query Match             56.6%;  Score 52.6;  DB 3;  Length 102;
  Best Local Similarity   53.8%;  Pred. No. 1.1e-08;
  Matches   49;  Conservative   18;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      : :||||:|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 11
US-08-689-190-1
; Sequence 1, Application US/08689190
; Patent No. 5714349
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  OSHIKA, Yuri
;    APPLICANT:  YAMADA, Takao
;    TITLE OF INVENTION:  SYNTHETIC GENE CODING FOR HUMAN
;    TITLE OF INVENTION:  PARATHYROID HORMONE
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/689,190
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/006,197
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/016,171
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/765,371
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILLIAMS, Gregory D
;      REGISTRATION NUMBER:  30,901
;      REFERENCE/DOCKET NUMBER:  41,288
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthesizing DNA
```

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;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..252
;      IDENTIFICATION METHOD:  E
;    FEATURE:
;      NAME/KEY:  MUTATION
;      LOCATION:  7, 8, 9, 12, 15, 19, 21, 33, 36, 43, 51, 58, 60,
;      IDENTIFICATION METHOD:  S
US-08-689-190-1

  Query Match             56.6%;  Score 52.6;  DB 2;  Length 252;
  Best Local Similarity   53.8%;  Pred. No. 1.4e-08;
  Matches   49;  Conservative   18;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      : :||||:|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 12
US-08-733-446-23
; Sequence 23, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid,  synthetic DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..252
;      IDENTIFICATION METHOD:  E
US-08-733-446-23

  Query Match             56.6%;  Score 52.6;  DB 2;  Length 252;
  Best Local Similarity   53.8%;  Pred. No. 1.4e-08;
  Matches   49;  Conservative   18;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      : :||||:|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 13
US-08-733-446-56
; Sequence 56, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..252
;      NAME/KEY:  mutation
;      LOCATION:  103...105
;      IDENTIFICATION METHOD:  E
US-08-733-446-56

  Query Match             56.6%;  Score 52.6;  DB 2;  Length 252;
  Best Local Similarity   53.8%;  Pred. No. 1.4e-08;
  Matches   49;  Conservative   18;  Mismatches   24;  Indels    0;  Gaps    0;
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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      : :||||:|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 14
US-08-835-231-34
; Sequence 34, Application US/08835231
; Patent No. 5861284
;  GENERAL INFORMATION:
;    APPLICANT:  NISHIMURA, Osamu
;    APPLICANT:  KURIYAMA, Masato
;    APPLICANT:  KOYAMA, No. 5861284uyuki
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  METHOD FOR PRODUCING A BIOLOGICALLY
;    TITLE OF INVENTION:  ACTIVE RECOMBINANT CYSTEINE-FREE
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/835,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,709
;      FILING DATE:  07-DEC-1994
;      APPLICATION NUMBER:  07/838,857
;      FILING DATE:  18-FEB-1992
;      APPLICATION NUMBER:  JP 024841
;      FILING DATE:  19-FEB-1991
;      APPLICATION NUMBER:  JP 0271438
;      FILING DATE:  18-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  41614-FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Synthetic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Synthetic DNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...252
US-08-835-231-34

  Query Match             56.6%;  Score 52.6;  DB 2;  Length 252;
  Best Local Similarity   53.8%;  Pred. No. 1.4e-08;
  Matches   49;  Conservative   18;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      : :||||:|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 15
US-09-108-661-34
; Sequence 34, Application US/09108661
; Patent No. 6287806
;  GENERAL INFORMATION:
;    APPLICANT:  NISHIMURA, Osamu
;    APPLICANT:  KURIYAMA, Masato
;    APPLICANT:  KOYAMA, No. 6287806uyuki
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  METHOD FOR PRODUCING A BIOLOGICALLY
;    TITLE OF INVENTION:  ACTIVE RECOMBINANT CYSTEINE-FREE
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/108,661
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,709
;      FILING DATE:  07-DEC-1994
;      APPLICATION NUMBER:  07/838,857
;      FILING DATE:  18-FEB-1992
;      APPLICATION NUMBER:  JP 024841
;      FILING DATE:  19-FEB-1991
;      APPLICATION NUMBER:  JP 0271438
;      FILING DATE:  18-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  41614-FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Synthetic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Synthetic DNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...252
US-09-108-661-34
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Query Match 56.6%; Score 52.6; DB 3; Length 252;
Best Local Similarity 53.8%; Pred. No. 1.4e-08;
Matches 49; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||       : :||||:|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92
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Search completed: November 24, 2005, 01:34:14
Job time : 74.6667 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 23:59:22 ; Search time 412.667 Seconds
(without alignments)
1863.616 Million cell updates/sec

Title: US-09-475-158A-14
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	69.6	74.8	102	9	US-10-997-078-60	Sequence 60, Appl
2	69.6	74.8	102	9	US-10-997-700-33	Sequence 33, Appl
3	69.6	74.8	111	9	US-10-997-078-61	Sequence 61, Appl
4	69.6	74.8	111	9	US-10-997-700-34	Sequence 34, Appl
5	69.6	74.8	117	9	US-10-997-078-141	Sequence 141, App
6	69.6	74.8	252	9	US-10-997-078-62	Sequence 62, Appl
7	69.6	74.8	252	9	US-10-997-700-35	Sequence 35, Appl
8	69.6	74.8	264	9	US-10-997-700-89	Sequence 89, Appl
9	69.6	74.8	276	9	US-10-997-762-18	Sequence 18, Appl
10	69.6	74.8	276	9	US-10-997-822-3	Sequence 3, Appli
11	69.6	74.8	276	9	US-10-997-700-75	Sequence 75, Appl
12	69.6	74.8	282	9	US-10-997-078-133	Sequence 133, App
13	69.6	74.8	291	9	US-10-997-700-76	Sequence 76, Appl
14	69.6	74.8	291	9	US-10-997-700-77	Sequence 77, Appl
15	69.6	74.8	321	9	US-10-997-700-91	Sequence 91, Appl
16	69.6	74.8	420	9	US-10-997-700-93	Sequence 93, Appl
17	69.6	74.8	426	9	US-10-997-762-20	Sequence 20, Appl
18	68	73.1	489	6	US-10-117-109-14	Sequence 14, Appl
19	68	73.1	489	6	US-10-407-078-14	Sequence 14, Appl
20	68	73.1	489	6	US-10-407-078-43	Sequence 43, Appl
21	57.4	61.7	717	8	US-10-848-279-7	Sequence 7, Appli
22	57.4	61.7	945	8	US-10-848-279-8	Sequence 8, Appli
23	53.8	57.8	106	3	US-09-746-945-11	Sequence 11, Appl
c 24	53.8	57.8	107	3	US-09-746-945-12	Sequence 12, Appl
25	53.6	57.6	348	6	US-10-437-038-1	Sequence 1, Appli
26	53.6	57.6	348	6	US-10-359-091-1	Sequence 1, Appli
27	53.6	57.6	432	6	US-10-437-038-3	Sequence 3, Appli
28	53.6	57.6	432	6	US-10-359-091-3	Sequence 3, Appli
29	53.6	57.6	874	6	US-10-437-038-7	Sequence 7, Appli
30	53.6	57.6	874	6	US-10-359-091-7	Sequence 7, Appli
31	52.6	56.6	102	6	US-10-340-484-14	Sequence 14, Appl
32	51	54.8	258	8	US-10-343-189-15	Sequence 15, Appl
33	47.8	51.4	102	9	US-10-775-204-24	Sequence 24, Appl
34	47.8	51.4	102	9	US-10-775-204-25	Sequence 25, Appl
35	47.8	51.4	102	9	US-10-775-204-51	Sequence 51, Appl
36	47.8	51.4	102	9	US-10-775-204-52	Sequence 52, Appl
37	47.8	51.4	102	9	US-10-775-204-57	Sequence 57, Appl
38	47.8	51.4	102	9	US-10-775-204-60	Sequence 60, Appl
39	47.8	51.4	102	9	US-10-775-204-61	Sequence 61, Appl
40	47.8	51.4	102	9	US-10-775-204-64	Sequence 64, Appl
41	47.8	51.4	102	9	US-10-775-204-69	Sequence 69, Appl
42	47.8	51.4	102	9	US-10-775-204-72	Sequence 72, Appl
43	47.8	51.4	102	9	US-10-775-204-1434	Sequence 1434, Ap
44	47.8	51.4	102	9	US-10-775-204-1435	Sequence 1435, Ap
45	47.8	51.4	201	9	US-10-775-204-1386	Sequence 1386, Ap

ALIGNMENTS

RESULT 1
US-10-997-078-60
; Sequence 60, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
; APPLICANT: Restoragen, Inc.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
; FILE REFERENCE: 1627.010US1
; CURRENT APPLICATION NUMBER: US/10/997,078
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16643
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,370
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PTH(1-34).
US-10-997-078-60

Query Match 74.8%; Score 69.6; DB 9; Length 102;
Best Local Similarity 63.0%; Pred. No. 2.6e-15;
Matches 58; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

```
Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:|||| ||: |:||||:| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
```

RESULT 2
US-10-997-700-33
; Sequence 33, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:

```
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 102
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-34).
US-10-997-700-33

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 102;
  Best Local Similarity   63.0%;  Pred. No. 2.6e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:|||       ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 3
US-10-997-078-61
; Sequence 61, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 111
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-37).
US-10-997-078-61

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 111;
  Best Local Similarity   63.0%;  Pred. No. 2.7e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:|||       ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 4
US-10-997-700-34
; Sequence 34, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 111
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-37).
US-10-997-700-34

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 111;
  Best Local Similarity   63.0%;  Pred. No. 2.7e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:|||       ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 5
US-10-997-078-141
; Sequence 141, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
;   LENGTH: 117
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PTH sequence.
US-10-997-078-141

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 117;
  Best Local Similarity   63.0%;  Pred. No. 2.7e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:|||       ||:      |:||||:| |:|||||:|
```

```
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 6
US-10-997-078-62
; Sequence 62, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
;   LENGTH: 252
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-84).
US-10-997-078-62

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 252;
  Best Local Similarity   63.0%;  Pred. No. 3.3e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 7
US-10-997-700-35
; Sequence 35, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 252
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-84).
US-10-997-700-35

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 252;
  Best Local Similarity   63.0%;  Pred. No. 3.3e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 8
US-10-997-700-89
; Sequence 89, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
;   LENGTH: 264
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic pBN121-M-PTH(1-84).
US-10-997-700-89

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 264;
  Best Local Similarity   63.0%;  Pred. No. 3.4e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:||||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         65 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 96


RESULT 9
US-10-997-762-18
; Sequence 18, Application US/10997762
; Publication No. US20050227313A1
; GENERAL INFORMATION:
;  APPLICANT: Seo, Jin Seog
;  APPLICANT:  Strydom, Daniel
;  APPLICANT:  Holmquist, Barton
;  APPLICANT:  Restoragen Inc.
;  TITLE OF INVENTION: Polypeptide Cleavage Process
;  FILE REFERENCE: 1627.026US1
;  CURRENT APPLICATION NUMBER: US/10/997,762
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16468
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,488
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 276
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence of a chimeric synthetic protein
US-10-997-762-18

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 276;
  Best Local Similarity   63.0%;  Pred. No. 3.4e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:|||||:|
Db        173 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 232

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264


RESULT 10
US-10-997-822-3
; Sequence 3, Application US/10997822
; Publication No. US20050227314A1
; GENERAL INFORMATION:
;  APPLICANT: Holmquist, B.
;  APPLICANT:  Strydom, D.
;  APPLICANT:  Gensalk, X.
;  APPLICANT:  Cryer, R.
;  TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
;  FILE REFERENCE: 1627.011US1
;  CURRENT APPLICATION NUMBER: US/10/997,822
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16647
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,484
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 276
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence of a synthetic chimeric protein.
US-10-997-822-3

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 276;
  Best Local Similarity   63.0%;  Pred. No. 3.4e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:|||||:|
Db        173 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 232

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264


RESULT 11
US-10-997-700-75
; Sequence 75, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
;   LENGTH: 276
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PCR product.
US-10-997-700-75

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 276;
  Best Local Similarity   63.0%;  Pred. No. 3.4e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:|||||:|
Db         14 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 73

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         74 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 105


RESULT 12
US-10-997-078-133
; Sequence 133, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
;   LENGTH: 282
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic sequence for the T7tagVg-PTH(1-34) cassette.
US-10-997-078-133

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 282;
  Best Local Similarity   63.0%;  Pred. No. 3.4e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:|||||:|
Db        167 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 226

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        227 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 258


RESULT 13
US-10-997-700-76
; Sequence 76, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
```

```
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 291
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PCR product.
US-10-997-700-76

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 291;
  Best Local Similarity   63.0%;  Pred. No. 3.4e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:||||||:|
Db         29 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 88

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         89 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 120


RESULT 14
US-10-997-700-77
; Sequence 77, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
;   LENGTH: 291
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PCR product.
US-10-997-700-77

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 291;
  Best Local Similarity   63.0%;  Pred. No. 3.4e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:||||||:|
Db         29 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 88

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         89 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 120


RESULT 15
US-10-997-700-91
; Sequence 91, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic pBN121-T7tag-CH-PTH(1-84).
US-10-997-700-91

  Query Match             74.8%;  Score 69.6;  DB 9;  Length 321;
  Best Local Similarity   63.0%;  Pred. No. 3.5e-15;
  Matches   58;  Conservative   20;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:      |:||||:| |:||||||:|
Db         62 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 121

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        122 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 153


Search completed: November 24, 2005, 04:46:55
Job time : 412.667 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 24, 2005, 01:30:39 ; Search time 195 Seconds
(without alignments)
70.875 Million cell updates/sec

Title: US-09-475-158A-14
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3205263 seqs, 74304013 residues

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	26.8	28.8	1410	7	US-11-167-273-2	Sequence 2, Appli
c	2	25.2	27.1	2327	1	US-10-821-234-760	Sequence 760, App
	3	24	25.8	2748	1	US-10-526-731-4	Sequence 4, Appli
c	4	23.4	25.2	1291	7	US-11-184-005-23	Sequence 23, Appl
	5	23.2	24.9	4053	1	US-10-131-826A-351	Sequence 351, App
	6	22.8	24.5	2206	1	US-10-510-386-67	Sequence 67, Appl
c	7	22.4	24.1	320	9	US-11-033-764-35	Sequence 35, Appl
	8	22.4	24.1	11438	1	US-10-821-234-224	Sequence 224, App
	9	22.2	23.9	1461	9	US-11-082-389-315	Sequence 315, App
	10	21.8	23.4	1209	7	US-11-074-176-353	Sequence 353, App
	11	21.8	23.4	1224	7	US-11-074-176-185	Sequence 185, App
c	12	21.8	23.4	2536	1	US-10-793-626-4301	Sequence 4301, Ap
c	13	21.6	23.2	1759	1	US-10-821-234-748	Sequence 748, App
	14	21.4	23.0	3901	1	US-10-821-234-112	Sequence 112, App
	15	21.2	22.8	459	1	US-10-821-234-598	Sequence 598, App
	16	21.2	22.8	459	1	US-10-821-234-725	Sequence 725, App
	17	21.2	22.8	477	1	US-10-842-206-19	Sequence 19, Appl
	18	21.2	22.8	477	1	US-10-980-459-3	Sequence 3, Appli
	19	21.2	22.8	567	1	US-10-980-459-31	Sequence 31, Appl
	20	21.2	22.8	594	1	US-10-980-459-29	Sequence 29, Appl
	21	21.2	22.8	603	1	US-10-980-459-27	Sequence 27, Appl
	22	21.2	22.8	612	1	US-10-980-459-25	Sequence 25, Appl
	23	21.2	22.8	630	1	US-10-980-459-23	Sequence 23, Appl
	24	21.2	22.8	636	1	US-10-842-206-1	Sequence 1, Appli
	25	21.2	22.8	636	1	US-10-980-459-8	Sequence 8, Appli
c	26	21.2	22.8	1910	1	US-10-821-234-211	Sequence 211, App
c	27	20.8	22.4	11337	1	US-10-499-715-1	Sequence 1, Appli
	28	20.6	22.2	7893	7	US-11-186-731-3	Sequence 3, Appli
	29	20.6	22.2	8106	7	US-11-186-731-1	Sequence 1, Appli
	30	20.6	22.2	23907	7	US-11-186-731-6	Sequence 6, Appli
	31	20.6	22.2	24120	7	US-11-186-731-4	Sequence 4, Appli
c	32	20.4	21.9	867	9	US-11-033-764-19	Sequence 19, Appl
	33	20.4	21.9	1189	1	US-10-821-234-83	Sequence 83, Appl
	34	20.4	21.9	5506	1	US-10-821-234-277	Sequence 277, App
c	35	20.4	21.9	5510	7	US-11-150-406-1	Sequence 1, Appli
	36	20.2	21.7	1208	1	US-10-821-234-290	Sequence 290, App
c	37	20.2	21.7	1359	1	US-10-858-730-53	Sequence 53, Appl
	38	20.2	21.7	1606	1	US-10-131-826A-65	Sequence 65, Appl
	39	20.2	21.7	1606	1	US-10-131-826A-257	Sequence 257, App
	40	20.2	21.7	5412	1	US-10-821-234-36	Sequence 36, Appl
	41	20.2	21.7	40439	1	US-10-993-509-1	Sequence 1, Appli
	42	20	21.5	809	8	US-11-132-839-6	Sequence 6, Appli
c	43	20	21.5	1542	1	US-10-990-276-4	Sequence 4, Appli
	44	20	21.5	1929	1	US-10-821-234-50	Sequence 50, Appl
	45	20	21.5	3719	1	US-10-131-826A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-11-167-273-2
; Sequence 2, Application US/11167273
; Publication No. US20050255567A1
; GENERAL INFORMATION:
; APPLICANT: GUSYATINER, Mikhail Markovich
; APPLICANT: IVANOVSKAYA, Lirina Valerievna
; APPLICANT: LEONOVA, Tatyana Viktorovna
; APPLICANT: MUKHANOVA, Ekaterina Igorevna
; APPLICANT: ROSTOVA, Yulia Georgievna
; APPLICANT: FILIPPOV, Dmitriy Vladmirovich
; APPLICANT: CHUDAKOVA, Daria Aleksandrovna
; TITLE OF INVENTION: NEW MUTANT GLUTAMINE SYNTHETASE AND METHOD FR PRODUCING AMINO ACI
; FILE REFERENCE: 230720US0
; CURRENT APPLICATION NUMBER: US/11/167,273
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: US/10/299,799
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: RU 2001132473
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-167-273-2

Query Match 28.8%; Score 26.8; DB 7; Length 1410;
Best Local Similarity 46.2%; Pred. No. 0.79;
Matches 36; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

```
Qy         15 CCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCG 74
              || ||:||:|  |||:  :| :||:     ||||   |:  | | |  |||    :|
Db       1122 CCTGCTGATGGCCGGTCTTGATGGTATCAAGAACAAGATCCATCCGGGCGAAGCCATGGA 1181

Qy         75 UAAAAAACUGCAGGACGU 92
                |||| |:| | ||| :
Db       1182 CAAAAACCTGTATGACCT 1199
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RESULT 2
US-10-821-234-760/c
; Sequence 760, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:

```
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 760
;   LENGTH: 2327
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-760

  Query Match             27.1%;  Score 25.2;  DB 1;  Length 2327;
  Best Local Similarity   43.6%;  Pred. No. 3.3;
  Matches   34;  Conservative   11;  Mismatches   33;  Indels    0;  Gaps    0;

Qy         16 CAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGU 75
              ||||:| :|| |   ||:||:|| ||      || |    || | :| :|   |  :  |:
Db        894 CAGCTGCTGCCCCTGGGTGGTGGAGGCGGTGACGCTGACGACCATGATGGTGGCATTGGT 835

Qy         76 AAAAAACUGCAGGACGUU 93
                |  | |:|| | | |::
Db        834 GAGGATCTGCTGCAGGTT 817


RESULT 3
US-10-526-731-4
; Sequence 4, Application US/10526731
; Publication No. US20050244437A1
; GENERAL INFORMATION:
;  APPLICANT: AKZO Nobel N.V.
;  TITLE OF INVENTION: live attenuated parasite vaccine
;  FILE REFERENCE: 2002-017-EP
;  CURRENT APPLICATION NUMBER: US/10/526,731
;  CURRENT FILING DATE:  2005-03-04
;  PRIOR APPLICATION NUMBER: EP 02078953
;  PRIOR FILING DATE: 2002-09-20
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 2748
;   TYPE: DNA
;   ORGANISM: Toxoplasma gondii
US-10-526-731-4

  Query Match             25.8%;  Score 24;  DB 1;  Length 2748;
  Best Local Similarity   54.2%;  Pred. No. 9.3;
  Matches   26;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         38 GUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGC 85
              |:||:|:|  | |||:|| ||  |  |||: | :|||  | || |: |
Db       2021 GTGGTCTGTGCGCCATGGCACAGGCAGAATCGTTGCGGTACAAGCTTC 2068


RESULT 4
US-11-184-005-23/c
; Sequence 23, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
;  APPLICANT: Luyten, Frank P.
;  APPLICANT:  Moos, Malcolm JR.
;  APPLICANT:  Hoang, Bang
;  APPLICANT:  Wang, Shouwen
;  TITLE OF INVENTION: METHOD OF MODULATING TISSUE
;  TITLE OF INVENTION:  GROWTH USING FRZB PROTEIN
;  FILE REFERENCE: NIH133.1CPC3
;  CURRENT APPLICATION NUMBER: US/11/184,005
;  CURRENT FILING DATE:  2005-07-18
;  PRIOR APPLICATION NUMBER: US 10/028051
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US 08/822333
;  PRIOR FILING DATE: 1997-03-20
;  PRIOR APPLICATION NUMBER: US 08/729,452
;  PRIOR FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 1291
;   TYPE: DNA
;   ORGANISM: Xenopus laevis
US-11-184-005-23

  Query Match             25.2%;  Score 23.4;  DB 7;  Length 1291;
  Best Local Similarity   40.4%;  Pred. No. 13;
  Matches   36;  Conservative   12;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||: ::  | | |: |||    :|| | |:    |        : |||: | :|||||
Db       1274 GCTCTTAGCTACATTCAGTCACTGCTCTGTCACTGGAAGTTGATAAACTGCCTGGAACAC 1215

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGA 89
              |:  ||:       :||||||  | ||||
Db       1214 GTGCAATATAGTTATAAAAAAAAGAAGGA 1186


RESULT 5
US-10-131-826A-351
; Sequence 351, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C128
;  CURRENT APPLICATION NUMBER: US/10/131,826A
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
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;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 351
;   LENGTH: 4053
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-131-826A-351

  Query Match             24.9%;  Score 23.2;  DB 1;  Length 4053;
  Best Local Similarity   40.5%;  Pred. No. 20;
  Matches   34;  Conservative   12;  Mismatches   38;  Indels    0;  Gaps    0;

Qy         10 GAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGG 69
              | ||   | |: |:| | || | :  : | || |:|| |  ||:||||  : :  |   |
Db        997 GTAACGAAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAACATGGAAATTTTGCAGCTG 1056

Qy         70 CUGCGUAAAAAACUGCAGGACGUU 93
                | :|| || |:    ||  ::
Db        1057 GACCATAACAACCTAACAGAGATT 1080


RESULT 6
US-10-510-386-67
; Sequence 67, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
;  APPLICANT: Andersen, Jens Tonne
;  APPLICANT:  Clausen, Ib Groth
;  APPLICANT:  Jorgensen, Steen Troels
;  APPLICANT:  Olsen, Peter Bjarke
;  APPLICANT:  Rasmussen, Michael Dolberg
;  TITLE OF INVENTION: Improved Bacillus Host Cell
;  FILE REFERENCE: 10294.204-US
;  CURRENT APPLICATION NUMBER: US/10/510,386
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 248
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
;   LENGTH: 2206
;   TYPE: DNA
;   ORGANISM: Bacillus licheniformis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (501)..(1703)
US-10-510-386-67

  Query Match             24.5%;  Score 22.8;  DB 1;  Length 2206;
  Best Local Similarity   44.6%;  Pred. No. 24;
  Matches   33;  Conservative    9;  Mismatches   32;  Indels    0;  Gaps    0;

Qy         14 UCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGC 73
              :|   |:||:|    |  |  ||:|  ||  :|||| | |  ||||   ::||  |  :
Db        559 TCTGCCTGATGATTGAAGCGGGTGCGGGAATGAACACGACTGAACAGTTTGAGAGCTTAT 618

Qy         74 GUAAAAAACUGCAG 87
              :|||||   || |
Db        619 TTAAAAACAGGCCG 632


RESULT 7
US-11-033-764-35/c
; Sequence 35, Application US/11033764
; Publication No. US20050244817A1
; GENERAL INFORMATION:
;  APPLICANT: Rubin, Donald H.
;  APPLICANT:  Organ, Edward L.
;  APPLICANT:  DuBois, Raymond N.
;  TITLE OF INVENTION: Mammalian Genes Involved in Viral
;  TITLE OF INVENTION:  Infection and Tumor Suppression
;  FILE REFERENCE: 01123.0004
;  CURRENT APPLICATION NUMBER: US/11/033,764
;  CURRENT FILING DATE:  2005-01-12
;  PRIOR APPLICATION NUMBER: US/10/877,807
;  PRIOR FILING DATE: 2004-06-25
;  PRIOR APPLICATION NUMBER: US/09/509,712
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: PCT/US98/21276
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/062,021
;  PRIOR FILING DATE: 1997-10-10
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 320
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1- 320
;   OTHER INFORMATION: n = g, a, c or t(u)
US-11-033-764-35

  Query Match             24.1%;  Score 22.4;  DB 9;  Length 320;
  Best Local Similarity   43.8%;  Pred. No. 20;
  Matches   28;  Conservative   10;  Mismatches   26;  Indels    0;  Gaps    0;

Qy         13 AUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUG 72
              | ||||   |: | | |   :||:   || |:| ||: |   || | :|:   |:|| :|
Db         64 AACCAGTGTATACTCTGCCATGGTCCAGGCCTGTACTTCTGTGATCTTGTGTCATGGGTG 5

Qy         73 CGUA 76
              | :|
Db          4 CATA 1


RESULT 8
US-10-821-234-224
; Sequence 224, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 224
;   LENGTH: 11438
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-224

  Query Match             24.1%;  Score 22.4;  DB 1;  Length 11438;
  Best Local Similarity   47.2%;  Pred. No. 51;
  Matches   34;  Conservative    7;  Mismatches   31;  Indels    0;  Gaps    0;

Qy         15 CCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCG 74
              |||||:| :|  ||  ||    || || |:  ||:  | | | | :| :|   | | | |
Db       3886 CCAGCTGCTGTGCGTGGGCCTCGGCGGCCTCCACTAGACGCAGCTTGCTGCCCGCCGGGG 3945

Qy         75 UAAAAAACUGCA 86
                ||   |:|||
Db       3946 AGAAGGTCTGCA 3957


RESULT 9
US-11-082-389-315
; Sequence 315, Application US/11082389
```

```
; Publication No. US20050244935A1
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-131CPCN
;  CURRENT APPLICATION NUMBER: US/11/082,389
;  CURRENT FILING DATE:  2005-03-16
;  PRIOR APPLICATION NUMBER: US 09/603024
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: US 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 60/143262
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: US 60/151281
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19930487.4
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: DE 19930489.0
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: DE 19931549.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931550.7
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932134.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19941379.7
;  PRIOR FILING DATE: 1999-08-31
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 315
;   LENGTH: 1461
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(1438)
;   OTHER INFORMATION: RXN01995
US-11-082-389-315

  Query Match             23.9%;  Score 22.2;  DB 9;  Length 1461;
  Best Local Similarity   45.1%;  Pred. No. 35;
  Matches   23;  Conservative   10;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          4 GUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUG 54
              |::  ||    |  ||:||:  | ||: |:|  | :|||:|:| || || :|
Db       1148 GTTGTCGTGGGCATGCTGATCAATGGTTGTGTGGCTGGTCTGTACACCCTG 1198


RESULT 10
US-11-074-176-353
; Sequence 353, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
;  APPLICANT: Klaenhammer, Todd R.
;  APPLICANT:  Russell, William M.
;  APPLICANT:  Altermann, Eric
;  APPLICANT:  McAuliffe, Olivia
;  APPLICANT:  Peril, Andrea Azcarate
;  TITLE OF INVENTION: Nucleic Acid Sequences Encoding
;  TITLE OF INVENTION:  Stress-Related Proteins and Uses Therefore
;  FILE REFERENCE: 5051-694
;  CURRENT APPLICATION NUMBER: US/11/074,176
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: 60/551,161
;  PRIOR FILING DATE: 2004-03-08
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 353
;   LENGTH: 1209
;   TYPE: DNA
;   ORGANISM: Lactobacillus acidophilus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1209)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: ORF 699; phosphoglycerate kinase
US-11-074-176-353

  Query Match             23.4%;  Score 21.8;  DB 7;  Length 1209;
  Best Local Similarity   44.9%;  Pred. No. 46;
  Matches   22;  Conservative   10;  Mismatches   17;  Indels    0;  Gaps    0;

Qy         28 GGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUA 76
              ||:||:||:| :   |: |||: | : ||| |:   | |: ||   |:|
Db       1141 GGTGGTGGTGCTTCACTTAACTACCTTGAAGGTAAAGTATTGCCAGGTA 1189


RESULT 11
US-11-074-176-185
; Sequence 185, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
;  APPLICANT: Klaenhammer, Todd R.
;  APPLICANT:  Russell, William M.
;  APPLICANT:  Altermann, Eric
;  APPLICANT:  McAuliffe, Olivia
;  APPLICANT:  Peril, Andrea Azcarate
;  TITLE OF INVENTION: Nucleic Acid Sequences Encoding
;  TITLE OF INVENTION:  Stress-Related Proteins and Uses Therefore
;  FILE REFERENCE: 5051-694
;  CURRENT APPLICATION NUMBER: US/11/074,176
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: 60/551,161
;  PRIOR FILING DATE: 2004-03-08
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 185
;   LENGTH: 1224
;   TYPE: DNA
;   ORGANISM: Lactobacillus acidophilus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1224)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: ORF 699; phosphoglycerate kinase
US-11-074-176-185

  Query Match             23.4%;  Score 21.8;  DB 7;  Length 1224;
  Best Local Similarity   44.9%;  Pred. No. 46;
  Matches   22;  Conservative   10;  Mismatches   17;  Indels    0;  Gaps    0;

Qy         28 GGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUA 76
              ||:||:||:| :   |: |||: | : ||| |:   | |: ||   |:|
Db       1156 GGTGGTGGTGCTTCACTTAACTACCTTGAAGGTAAAGTATTGCCAGGTA 1204


RESULT 12
US-10-793-626-4301/c
; Sequence 4301, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
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;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4301
;    LENGTH: 2536
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: synthetic
;    OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4301

  Query Match             23.4%;  Score 21.8;  DB 1;  Length 2536;
  Best Local Similarity   44.9%;  Pred. No. 56;
  Matches   22;  Conservative   10;  Mismatches   17;  Indels    0;  Gaps    0;

Qy         33 UGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAA 81
              :||:  :||: :  ||:||| | || |  : | |:| |:|  :|  |||
Db       1705 TGGTTTTGGTTTCTACTCCAAGAAAGGAATAGCATGACTGATTATGAAA 1657


RESULT 13
US-10-821-234-748/c
; Sequence 748, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 748
;    LENGTH: 1759
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-821-234-748

  Query Match             23.2%;  Score 21.6;  DB 1;  Length 1759;
  Best Local Similarity   44.1%;  Pred. No. 60;
  Matches   30;  Conservative    9;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          7 UCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAA 66
              : ||  | ||  |:|  || |   | :||  | | :|:|||  |   ||   |: ::|||
Db        469 TTCGCTAGCCTCCTGCAGCGCACCGATGGCTGCGCTCTGAAACCTCAGGTCGGTTTTGAA 410

Qy         67 UGGCUGCG 74
                |:|||
Db        409 ATCCTGCG 402


RESULT 14
US-10-821-234-112
; Sequence 112, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 112
;    LENGTH: 3901
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-821-234-112

  Query Match             23.0%;  Score 21.4;  DB 1;  Length 3901;
  Best Local Similarity   38.0%;  Pred. No. 87;
  Matches   30;  Conservative   13;  Mismatches   36;  Indels    0;  Gaps    0;

Qy         14 UCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGC 73
              :|||| :||: ||   : |   :  : | |:  |   | :|||||   : |||:  | ||
Db       2374 TCCAGGTGATCCATCCTTGCCATCTTCGCCTTTAGCTCCTGGAACACCTGGAATACCAGC 2433

Qy         74 GUAAAAAACUGCAGGACGU 92
                : |     : ||  |||:
Db       2434 CTCACCGCGTTCACCACGT 2452


RESULT 15
US-10-821-234-598
; Sequence 598, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 598
;    LENGTH: 459
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-821-234-598

  Query Match             22.8%;  Score 21.2;  DB 1;  Length 459;
  Best Local Similarity   50.0%;  Pred. No. 58;
  Matches   29;  Conservative    6;  Mismatches   23;  Indels    0;  Gaps    0;

Qy         14 UCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCU 71
              :|| ||:|| || | |  | || || |  | || |   |:||  ||:  :| |  ||:
Db         17 TCCTGCTGAAGCCCTGGTGGGGAGGGGCACAGAGCGAGATGGGGCGTAATGGAATGCT 74


Search completed: November 24, 2005, 04:56:47
Job time : 195 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:00:32 ; Search time 242.667 Seconds
(without alignments)
2554.189 Million cell updates/sec

Title: US-09-475-158A-15
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	93	3	AAA51730	Aaa51730 PTH funct
2	83.4	89.7	93	3	AAA51729	Aaa51729 PTH funct
3	64.2	69.0	93	3	AAA51731	Aaa51731 PTH funct
4	61.6	66.2	152	2	AAT73910	Aat73910 Synthetic
5	60	64.5	102	12	ADG93179	Adg93179 Novel exp
6	60	64.5	102	12	ADJ65857	Adj65857 PTH pepti
7	60	64.5	102	13	ADW14377	Adw14377 Human par
8	60	64.5	111	12	ADG93180	Adg93180 Novel exp
9	60	64.5	111	12	ADJ65858	Adj65858 PTH pepti
10	60	64.5	111	13	ADW14375	Adw14375 Human par
11	60	64.5	117	12	ADG93260	Adg93260 Novel exp
12	60	64.5	168	2	AAT34865	Aat34865 Plasmid p
13	60	64.5	252	12	ADG93181	Adg93181 Novel exp
14	60	64.5	252	12	ADJ65859	Adj65859 PTH prote
15	60	64.5	264	12	ADJ65913	Adj65913 Tandem po
16	60	64.5	276	12	ADF90345	Adf90345 Chimeric
17	60	64.5	276	12	ADJ65899	Adj65899 PTH DNA s
18	60	64.5	276	12	ADJ87051	Adj87051 Nucleotid
19	60	64.5	282	12	ADG93252	Adg93252 Novel exp
20	60	64.5	291	12	ADJ65901	Adj65901 PTH DNA s
21	60	64.5	291	12	ADJ65900	Adj65900 PTH DNA s
22	60	64.5	294	2	AAT34866	Aat34866 Plasmid p
23	60	64.5	321	12	ADJ65915	Adj65915 Tandem po
24	60	64.5	420	12	ADJ65917	Adj65917 Tandem po
25	60	64.5	426	12	ADF90347	Adf90347 Chimeric
26	60	64.5	528	6	AAS19702	Aas19702 DNA encod
27	58.4	62.8	108	13	ADV69494	Adv69494 Human par
28	58.4	62.8	114	13	ADV69502	Adv69502 Human par
29	58.4	62.8	489	12	ADG48030	Adg48030 Human PTH
30	58.4	62.8	489	12	ADG48059	Adg48059 Human PTH
31	58.4	62.8	489	12	ADG68786	Adg68786 Human mut
32	54.2	58.3	141	2	AAQ89920	Aaq89920 Recombina
33	54.2	58.3	141	2	AAT80383	Aat80383 rPTH codi
34	54.2	58.3	207	2	AAQ89923	Aaq89923 Expressio
35	52.6	56.6	145	13	ADW80822	Adw80822 DNA encod
36	51	54.8	728	2	AAQ55301	Aaq55301 Truncated
37	51	54.8	945	2	AAQ55302	Aaq55302 gp55-Asn-
38	50.4	54.2	405	3	AAA51452	Aaa51452 PCpB-RVR-
39	50.4	54.2	408	3	AAA51455	Aaa51455 PCpB-LVPR
40	50.4	54.2	408	3	AAA51454	Aaa51454 PCpB-IEGR
41	50.4	54.2	411	3	AAA51453	Aaa51453 PCpB-ALY-
42	50.4	54.2	414	3	AAA51459	Aaa51459 PCpB-APR-
43	50.4	54.2	417	3	AAA51456	Aaa51456 PCpB-VIPR
44	50.4	54.2	423	3	AAA51457	Aaa51457 PCpB-DQVD
45	50.4	54.2	435	3	AAA51458	Aaa51458 PCpB-DFIA

ALIGNMENTS

RESULT 1
AAA51730
ID AAA51730 standard; RNA; 93 BP.
XX
AC AAA51730;
XX
DT 31-OCT-2000 (first entry)
XX
DE PTH functional domain conjugate peptide PG7 coding sequence.
XX
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW resorption; remodeling; tether1; osteoporosis; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .93
FT /*tag= a
FT /product= "PG7"
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
DR P-PSDB; AAY96975.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.

```
XX
PS   Claim 14; Fig 1; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 93 BP; 19 A; 16 C; 33 G; 0 T; 25 U; 0 Other;

  Query Match             100.0%;  Score 93;  DB 3;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-20;
  Matches   93;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |||||||||||||||||||||||||||||||||
Db         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93


RESULT 2
AAA51729
ID   AAA51729 standard; RNA; 93 BP.
XX
AC   AAA51729;
XX
DT   31-OCT-2000  (first entry)
XX
DE   PTH functional domain conjugate peptide PG5 coding sequence.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .93
FT                   /*tag=  a
FT                   /product= "PG5"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   P-PSDB; AAY96973.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 14; Fig 1; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 93 BP; 21 A; 18 C; 30 G; 0 T; 24 U; 0 Other;

  Query Match             89.7%;  Score 83.4;  DB 3;  Length 93;
  Best Local Similarity   93.5%;  Pred. No. 4.6e-17;
  Matches   87;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |||||||||||||||||||||||||||||||||
Db         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93


RESULT 3
AAA51731
ID   AAA51731 standard; RNA; 93 BP.
XX
AC   AAA51731;
XX
DT   31-OCT-2000  (first entry)
XX
DE   PTH functional domain conjugate peptide PG9 coding sequence.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .93
FT                   /*tag=  a
FT                   /product= "PG9"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   P-PSDB; AAY96974.
```

```
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 14; Fig 1; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 93 BP; 18 A; 14 C; 35 G; 0 T; 26 U; 0 Other;

  Query Match             69.0%;  Score 64.2;  DB 3;  Length 93;
  Best Local Similarity   80.6%;  Pred. No. 7e-11;
  Matches   75;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60
              ||||||||||||||||  ||||||||||||||||      ||||||||||||
Db          1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ||||||||||||||||||||||||||||||||
Db         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93


RESULT 4
AAT73910
ID   AAT73910 standard; DNA; 152 BP.
XX
AC   AAT73910;
XX
DT   25-MAR-2003  (revised)
DT   30-JAN-1998  (first entry)
XX
DE   Synthetic oligonucleotide encoding linker and PTH 1-37.
XX
KW   Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein;
KW   recombinant production; endoproteinase LysC; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .4
FT                   /*tag=  b
FT                   /label= sticky_end
FT                   /note= "5' end of complementary strand overhangs 3' end
FT                   of present strand by sequence 5'-TCGA-3'"
FT   CDS             6. .152
FT                   /*tag=  a
XX
PN   WO9718314-A1.
XX
PD   22-MAY-1997.
XX
PF   06-NOV-1996;   96WO-EP004850.
XX
PR   16-NOV-1995;   95DE-01042702.
XX
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI   Kopetzki E;
XX
DR   WPI; 1997-289290/26.
DR   P-PSDB; AAW21946.
XX
PT   Recombinant production of peptide(s) as fusions with streptavidin
PT   attached via cleavable linker - especially for urotropin and parathyroid
PT   hormone production.
XX
PS   Example 2; Fig 2; 37pp; German.
XX
CC   The present sequence, which encodes a linker and the parathyroid hormone
CC   1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was
CC   ligated to the 2.9 kb NheI-HindIII fragment of pSAM-CORE, which contains
CC   the Met(13-139) streptavidin (SA) sequence, to give pSA-EK-PTH. pSA-EK-
CC   PTH and the LacIq repressor plasmid pUBS500 were used to transform E.
CC   coli K12 RM82. The transformants were grown, with IPTG induction, in
CC   medium containing kanamycin and ampilcilin. Cells were harvested, lysed
CC   and isolated inclusion bodies solubilised in guanidine hydrochloride, and
CC   renatured by dilution in pH 7 phosphate buffer. The solution was
CC   clarified and the supernatant concentrated and purified on a column of
CC   immobilised iminobiotin. The purified material was incubated with
CC   endoproteinase LysC and the PTH 1-37 fragment released, recovered by SA
CC   fragment removal on an iminobiotin column followed by chromatography on a
CC   fractogel and reverse phase HPLC. The endoproteinase LysC cleaves the
CC   fusion protein rapidly and completely, exclusively at the Lys residue in
CC   the linker, i.e. not at Lys residues in SA. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;

  Query Match             66.2%;  Score 61.6;  DB 2;  Length 152;
  Best Local Similarity   59.8%;  Pred. No. 5.4e-10;
  Matches   55;  Conservative   18;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              | |:::||||||:||||||:||:||||      ||:            :|||:||||||:|
Db         37 CCGTTTCCGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCCATGGAACGTG 96

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         97 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 128


RESULT 5
ADG93179
ID   ADG93179 standard; DNA; 102 BP.
XX
AC   ADG93179;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel expression cassette-related polypeptide-encoding DNA SeqID60.
XX
KW   expression cassette; high yield polypeptide production;
KW   tandem polypeptide; inclusion body; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100021-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016643.
XX
PR   24-MAY-2002; 2002US-0383370P.
XX
PA   (REST-) RESTORAGEN INC.
PA   (HARL/) HARLEY S.
XX
PI   Harley S,  Williams JA,  Luan P,  Xia Y;
XX
DR   WPI; 2004-035128/03.
```

```
DR   P-PSDB; ADG93159.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 60; 157pp; English.
XX
CC   This invention relates to a novel expression cassette and methods for
CC   high yield production of polypeptides. The cassette comprises an operably
CC   linked nucleic acid sequence, where the expression of the cassette
CC   produces a tandem polypeptide that forms an inclusion body when expressed
CC   in a cell. The expression cassette is useful for producing peptide and
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present sequence is that of
CC   a DNA sequence which encodes a polypeptide which may be produced using
CC   the expression cassette of the invention.
XX
SQ   Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 60;  DB 12;  Length 102;
  Best Local Similarity   57.6%;  Pred. No. 1.6e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 6
ADJ65857
ID   ADJ65857 standard; DNA; 102 BP.
XX
AC   ADJ65857;
XX
DT   06-MAY-2004  (first entry)
XX
DE   PTH peptide coding sequence #1.
XX
KW   expression cassette; tandem polypeptide; inclusion body;
KW   inclusion body fusion partner; PTH; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100022-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016645.
XX
PR   24-MAY-2002; 2002US-0383212P.
XX
PA   (REST-) RESTORAGEN INC.
XX
PI   Xia Y,  Peng L;
XX
DR   WPI; 2004-035129/03.
DR   P-PSDB; ADJ65837.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 33; 132pp; English.
XX
CC   The invention comprises an expression cassette which produces a tandem
CC   polypeptide that form an inclusion body when expressed in a cell. The
CC   expression cassette of the invention is useful for producing a peptide or
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present DNA sequence encodes
CC   a peptide which may be used in the construction of a tandem polypeptide
CC   of the invention.
XX
SQ   Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 60;  DB 12;  Length 102;
  Best Local Similarity   57.6%;  Pred. No. 1.6e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 7
ADW14377
ID   ADW14377 standard; DNA; 102 BP.
XX
AC   ADW14377;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human parathyroxin PTH 1-34 peptide encoding DNA SEQ ID NO:3.
XX
KW   ds; parathyroxin; recombinant protein; protein engineering.
XX
OS   Homo sapiens.
XX
PN   CN1424325-A.
XX
PD   18-JUN-2003.
XX
PF   12-DEC-2001; 2001CN-00142627.
XX
PR   12-DEC-2001; 2001CN-00142627.
XX
PA   (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.
XX
PI   Chen C,  Xiu C,  Li M;
XX
DR   WPI; 2004-099606/11.
DR   P-PSDB; ADW14378.
XX
PT   Production of reorganized human parathyroid hormone 1-34 peptide.
XX
PS   Disclosure; SEQ ID NO 3; 25pp; Chinese.
XX
CC   The invention relates to a novel process for preparing recombinant human
CC   parathyroxin 1-34 peptide, including such steps as culturing a host cell
CC   in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376),
CC   severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and
CC   separating and purifying PTH 1-34 peptide. The present sequence encodes
CC   the PTH 1-34 peptide.
XX
SQ   Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 60;  DB 13;  Length 102;
  Best Local Similarity   57.6%;  Pred. No. 1.6e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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```
RESULT 8
ADG93180
ID   ADG93180 standard; DNA; 111 BP.
XX
AC   ADG93180;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel expression cassette-related polypeptide-encoding DNA SeqID61.
XX
KW   expression cassette; high yield polypeptide production;
KW   tandem polypeptide; inclusion body; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100021-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016643.
XX
PR   24-MAY-2002; 2002US-0383370P.
XX
PA   (REST-) RESTORAGEN INC.
PA   (HARL/) HARLEY S.
XX
PI   Harley S,  Williams JA,  Luan P,  Xia Y;
XX
DR   WPI; 2004-035128/03.
DR   P-PSDB; ADG93160.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 61; 157pp; English.
XX
CC   This invention relates to a novel expression cassette and methods for
CC   high yield production of polypeptides. The cassette comprises an operably
CC   linked nucleic acid sequence, where the expression of the cassette
CC   produces a tandem polypeptide that forms an inclusion body when expressed
CC   in a cell. The expression cassette is useful for producing peptide and
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present sequence is that of
CC   a DNA sequence which encodes a polypeptide which may be produced using
CC   the expression cassette of the invention.
XX
SQ   Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 60;  DB 12;  Length 111;
  Best Local Similarity   57.6%;  Pred. No. 1.6e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:           :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 9
ADJ65858
ID   ADJ65858 standard; DNA; 111 BP.
XX
AC   ADJ65858;
XX
DT   06-MAY-2004  (first entry)
XX
DE   PTH peptide coding sequence #2.
XX
KW   expression cassette; tandem polypeptide; inclusion body;
KW   inclusion body fusion partner; PTH; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100022-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016645.
XX
PR   24-MAY-2002; 2002US-0383212P.
XX
PA   (REST-) RESTORAGEN INC.
XX
PI   Xia Y,  Peng L;
XX
DR   WPI; 2004-035129/03.
DR   P-PSDB; ADJ65838.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 34; 132pp; English.
XX
CC   The invention comprises an expression cassette which produces a tandem
CC   polypeptide that form an inclusion body when expressed in a cell. The
CC   expression cassette of the invention is useful for producing a peptide or
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present DNA sequence encodes
CC   a peptide which may be used in the construction of a tandem polypeptide
CC   of the invention.
XX
SQ   Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 60;  DB 12;  Length 111;
  Best Local Similarity   57.6%;  Pred. No. 1.6e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:           :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 10
ADW14375
ID   ADW14375 standard; DNA; 111 BP.
XX
AC   ADW14375;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human parathyroxin Gly-Ser-Pro-PTH 1-34 peptide DNA SEQ ID NO:1.
XX
KW   ds; parathyroxin; recombinant protein; protein engineering.
XX
OS   Homo sapiens.
XX
PN   CN1424325-A.
XX
PD   18-JUN-2003.
XX
PF   12-DEC-2001; 2001CN-00142627.
XX
PR   12-DEC-2001; 2001CN-00142627.
XX
PA   (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.
XX
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PI   Chen C,  Xiu C,  Li M;
XX
DR   WPI; 2004-099606/11.
DR   P-PSDB; ADW14376.
XX
PT   Production of reorganized human parathyroid hormone 1-34 peptide.
XX
PS   Claim 3; SEQ ID NO 1; 25pp; Chinese.
XX
CC   The invention relates to a novel process for preparing recombinant human
CC   parathyroxin 1-34 peptide, including such steps as culturing a host cell
CC   in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376),
CC   severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and
CC   separating and purifying PTH 1-34 peptide. The present sequence encodes
CC   the Gly-Ser-Pro-PTH 1-34 peptide.
XX
SQ   Sequence 111 BP; 31 A; 28 C; 25 G; 27 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 60;  DB 13;  Length 111;
  Best Local Similarity   57.6%;  Pred. No. 1.6e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db         11 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 70

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         71 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 102


RESULT 11
ADG93260
ID   ADG93260 standard; DNA; 117 BP.
XX
AC   ADG93260;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel expression cassette-related PTH DNA SeqID141.
XX
KW   expression cassette; high yield polypeptide production;
KW   tandem polypeptide; inclusion body; gene; ds; PTH.
XX
OS   Unidentified.
OS   Synthetic.
XX
PN   WO2003100021-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016643.
XX
PR   24-MAY-2002; 2002US-0383370P.
XX
PA   (REST-) RESTORAGEN INC.
PA   (HARL/) HARLEY S.
XX
PI   Harley S,  Williams JA,  Luan P,  Xia Y;
XX
DR   WPI; 2004-035128/03.
DR   P-PSDB; ADG93259.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 141; 157pp; English.
XX
CC   This invention relates to a novel expression cassette and methods for
CC   high yield production of polypeptides. The cassette comprises an operably
CC   linked nucleic acid sequence, where the expression of the cassette
CC   produces a tandem polypeptide that forms an inclusion body when expressed
CC   in a cell. The expression cassette is useful for producing peptide and
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present sequence is that of
CC   a DNA sequence which encodes a PTH peptide which was used in the
CC   exemplification of the invention.
XX
SQ   Sequence 117 BP; 35 A; 27 C; 25 G; 30 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 60;  DB 12;  Length 117;
  Best Local Similarity   57.6%;  Pred. No. 1.7e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 12
AAT34865
ID   AAT34865 standard; cDNA; 168 BP.
XX
AC   AAT34865;
XX
DT   02-DEC-1996  (first entry)
XX
DE   Plasmid pBN1:PTH(1-34)C-1c portion encoding PTH(1-34)Cys.
XX
KW   PTH; parathyroid hormone; parathormone; C-amide; C-amidated peptide;
KW   alpha-carboxamide; recombinant protein; fusion protein; transpeptidation;
KW   vector; plasmid pBN1; carbonic anhydrase II; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .162
FT                   /*tag=  a
FT                   /product= "hCA-linker-PTH(1-34)Cys fusion"
XX
PN   WO9617941-A2.
XX
PD   13-JUN-1996.
XX
PF   07-DEC-1995;   95WO-US015799.
XX
PR   07-DEC-1994;   94US-00350528.
XX
PA   (BION-) BIONEBRASKA INC.
XX
PI   Stout JS,  Patridge BE,  Heriksen DB,  Holmquist B,  Wagner FW;
XX
DR   WPI; 1996-287185/29.
DR   P-PSDB; AAR98967.
XX
PT   Production of C-terminal alpha-carboxamidated peptide(s) - by cleavage
PT   and transpeptidation of recombinant multicopy peptide(s) or fusion
PT   constructs.
XX
PS   Example 7; Fig 1; 93pp; English.
XX
CC   A portion (AAT34865) of plasmid pBN1:PTH(1-34)C-1c comprises DNA coding
CC   for a fusion protein (AAR87867) composed of the C-terminal end of human
CC   carbonic anhydrase II joined by an intraconnecting peptide (including a
CC   thrombin cleavage site) to amino acids 1-34 of PTH (AAR98966), followed
CC   by a Cys residue and C-terminal sequence. The complete construct can be
CC   expressed in E. coli transformants. The intraconnecting peptide and C-
CC   terminal Cys residue enable the recombinant protein construct to be
CC   selectively reacted to produce C-terminal carboxamidated PTH(1-34)
XX
SQ   Sequence 168 BP; 41 A; 44 C; 42 G; 41 T; 0 U; 0 Other;
```

```
  Query Match             64.5%;  Score 60;  DB 2;  Length 168;
  Best Local Similarity   57.6%;  Pred. No. 1.8e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db         47 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 106

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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Db        107 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 138


RESULT 13
ADG93181
ID   ADG93181 standard; DNA; 252 BP.
XX
AC   ADG93181;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel expression cassette-related polypeptide-encoding DNA SeqID62.
XX
KW   expression cassette; high yield polypeptide production;
KW   tandem polypeptide; inclusion body; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100021-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016643.
XX
PR   24-MAY-2002; 2002US-0383370P.
XX
PA   (REST-) RESTORAGEN INC.
PA   (HARL/) HARLEY S.
XX
PI   Harley S,  Williams JA,  Luan P,  Xia Y;
XX
DR   WPI; 2004-035128/03.
DR   P-PSDB; ADG93161.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 62; 157pp; English.
XX
CC   This invention relates to a novel expression cassette and methods for
CC   high yield production of polypeptides. The cassette comprises an operably
CC   linked nucleic acid sequence, where the expression of the cassette
CC   produces a tandem polypeptide that forms an inclusion body when expressed
CC   in a cell. The expression cassette is useful for producing peptide and
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present sequence is that of
CC   a DNA sequence which encodes a polypeptide which may be produced using
CC   the expression cassette of the invention.
XX
SQ   Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 60;  DB 12;  Length 252;
  Best Local Similarity   57.6%;  Pred. No. 2e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 14
ADJ65859
ID   ADJ65859 standard; DNA; 252 BP.
XX
AC   ADJ65859;
XX
DT   06-MAY-2004  (first entry)
XX
DE   PTH protein coding sequence.
XX
KW   expression cassette; tandem polypeptide; inclusion body;
KW   inclusion body fusion partner; PTH; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100022-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016645.
XX
PR   24-MAY-2002; 2002US-0383212P.
XX
PA   (REST-) RESTORAGEN INC.
XX
PI   Xia Y,  Peng L;
XX
DR   WPI; 2004-035129/03.
DR   P-PSDB; ADJ65839.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 35; 132pp; English.
XX
CC   The invention comprises an expression cassette which produces a tandem
CC   polypeptide that form an inclusion body when expressed in a cell. The
CC   expression cassette of the invention is useful for producing a peptide or
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present DNA sequence encodes
CC   a protein which may be used in the construction of a tandem polypeptide
CC   of the invention.
XX
SQ   Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;

  Query Match             64.5%;  Score 60;  DB 12;  Length 252;
  Best Local Similarity   57.6%;  Pred. No. 2e-09;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 15
ADJ65913
ID   ADJ65913 standard; DNA; 264 BP.
XX
AC   ADJ65913;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Tandem polypeptide-encoding expression cassette #6.
XX
KW   expression cassette; tandem polypeptide; inclusion body;
```

KW inclusion body fusion partner; gene; ds.
XX
OS Unidentified.
XX
PN WO2003100022-A2.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-US016645.
XX
PR 24-MAY-2002; 2002US-0383212P.
XX
PA (REST-) RESTORAGEN INC.
XX
PI Xia Y, Peng L;
XX
DR WPI; 2004-035129/03.
DR P-PSDB; ADJ65912.
XX
PT New expression cassette comprising an operably linked nucleic acid
PT sequence, useful for producing a tandem polypeptide that forms an
PT inclusion body when expressed in a cell.
XX
PS Disclosure; SEQ ID NO 89; 132pp; English.
XX
CC The invention comprises an expression cassette which produces a tandem
CC polypeptide that form an inclusion body when expressed in a cell. The
CC expression cassette of the invention is useful for producing a peptide or
CC polypeptide in a cell, preferably a tandem polypeptide that forms an
CC inclusion body when expressed in a cell. The present DNA sequence
CC represents an expression cassette which encodes a tandem polypeptide of
CC the invention.
XX
SQ Sequence 264 BP; 72 A; 67 C; 64 G; 61 T; 0 U; 0 Other;

Query Match 64.5%; Score 60; DB 12; Length 264;
Best Local Similarity 57.6%; Pred. No. 2e-09;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:        :| |:||||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         65 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 96
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Search completed: November 23, 2005, 23:00:14
Job time : 242.667 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:35:17 ; Search time 1177.67 Seconds
(without alignments)
4488.911 Million cell updates/sec

Title: US-09-475-158A-15
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	93	100.0	93	6	BD266833	BD266833 PTH funct
	2	83.4	89.7	93	6	BD266832	BD266832 PTH funct
	3	64.2	69.0	93	6	BD266834	BD266834 PTH funct
	4	56.8	61.1	258	6	AR269042	AR269042 Sequence
	5	54.2	58.3	141	6	AR005132	AR005132 Sequence
c	6	54.2	58.3	141	6	AR005133	AR005133 Sequence
	7	54.2	58.3	141	6	AR177779	AR177779 Sequence
c	8	54.2	58.3	141	6	AR177780	AR177780 Sequence
	9	54.2	58.3	207	6	AR043797	AR043797 Sequence
	10	51	54.8	717	6	A36847	A36847 Sequence 1
	11	51	54.8	945	6	A36849	A36849 Sequence 3
	12	50.4	54.2	405	6	BD234383	BD234383 Recombina
	13	50.4	54.2	408	6	BD234385	BD234385 Recombina
	14	50.4	54.2	408	6	BD234386	BD234386 Recombina
	15	50.4	54.2	411	6	BD234384	BD234384 Recombina
	16	50.4	54.2	414	6	BD234390	BD234390 Recombina
	17	50.4	54.2	417	6	BD234387	BD234387 Recombina
	18	50.4	54.2	423	6	BD234388	BD234388 Recombina
	19	50.4	54.2	435	6	BD234389	BD234389 Recombina
	20	46.2	49.7	252	6	AR027046	AR027046 Sequence
	21	46.2	49.7	252	6	E05675	E05675 DNA encodin
	22	44.6	48.0	252	6	AR027011	AR027011 Sequence
	23	44.6	48.0	252	6	AR027044	AR027044 Sequence
	24	44.6	48.0	252	6	AR030635	AR030635 Sequence
	25	44.6	48.0	252	6	AR168173	AR168173 Sequence
	26	44.6	48.0	252	6	E05658	E05658 DNA encodin
	27	44.6	48.0	252	6	E05673	E05673 DNA encodin
	28	44.6	48.0	252	6	I83594	I83594 Sequence 1
	29	44.6	48.0	263	6	AR027020	AR027020 Sequence
	30	44.6	48.0	263	6	E04335	E04335 Synthetic D
	31	44.6	48.0	263	6	E05671	E05671 DNA encodin
	32	44.6	48.0	263	6	I83595	I83595 Sequence 3
	33	44.6	48.0	263	11	S71759	S71759 human parat
c	34	44.6	48.0	265	6	AR027021	AR027021 Sequence
c	35	44.6	48.0	265	6	E05672	E05672 DNA encodin
c	36	44.6	48.0	265	6	I83596	I83596 Sequence 4
c	37	43.4	46.7	74	6	AR043802	AR043802 Sequence
	38	43	46.2	67	6	A79761	A79761 Sequence 9
	39	43	46.2	67	6	AR135774	AR135774 Sequence
	40	43	46.2	102	6	BD170195	BD170195 Process f
	41	43	46.2	186	6	BD170222	BD170222 Process f
	42	43	46.2	201	6	BD170213	BD170213 Process f
	43	43	46.2	225	6	BD170211	BD170211 Process f
	44	43	46.2	240	6	BD170198	BD170198 Process f
	45	43	46.2	252	6	AR027050	AR027050 Sequence

ALIGNMENTS

RESULT 1
BD266833
LOCUS BD266833 93 bp RNA linear PAT 17-JUL-2003
DEFINITION PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.
ACCESSION BD266833
VERSION BD266833.1 GI:33076601
KEYWORDS JP 2002533115-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 93)
AUTHORS Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
TITLE PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules
JOURNAL Patent: JP 2002533115-A 2 08-OCT-2002;
THE GENERAL HOSPITAL CORP
COMMENT OS Artificial Sequence
PN JP 2002533115-A/2
PD 08-OCT-2002
PF 30-DEC-1999 JP 2000591171
PR 31-DEC-1998 US 60/114577
PI THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD PI JUEPPNER
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC A61P19/10,
PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: modified PTH sequence FH Key Location/Qualifiers
FT source 1. .93
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .93
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ORIGIN

Query Match 100.0%; Score 93; DB 6; Length 93;

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  Best Local Similarity   73.1%;  Pred. No. 6.9e-17;
  Matches   68;  Conservative   25;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60
              ||:|:::|||||:|||||:||:||||||:||:||:||:||:||::|||:||||||:
Db          1 GCTGTTTCCGAAATCCAGCTGATGCACGGTGGTGGTGGTGGTGGTGGTTCCATGGAACGT 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |::|||:|||:|||:||||||||:||||||||::
Db         61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 2
BD266832
LOCUS       BD266832                 93 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules.
ACCESSION   BD266832
VERSION     BD266832.1  GI:33076600
KEYWORDS    JP 2002533115-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
  TITLE     PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules
  JOURNAL   Patent: JP 2002533115-A 1 08-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002533115-A/1
            PD   08-OCT-2002
            PF   30-DEC-1999 JP 2000591171
            PR   31-DEC-1998 US    60/114577
            PI   THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD  PI
            JUEPPNER
            PC   C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC
              A61P19/10,
            PC   A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
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ORIGIN

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  Best Local Similarity   68.8%;  Pred. No. 4.7e-14;
  Matches   64;  Conservative   23;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60
              ||:|:::|||||:|||||:||:|||||||:||:||:||:||:      :|||:||||||:
Db          1 GCTGTTTCCGAAATCCAGCTGATGCACGGTGGTGGTGGTGGTCTGAACTCCATGGAACGT 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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Db         61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 3
BD266834
LOCUS       BD266834                 93 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules.
ACCESSION   BD266834
VERSION     BD266834.1  GI:33076602
KEYWORDS    JP 2002533115-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
  TITLE     PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules
  JOURNAL   Patent: JP 2002533115-A 3 08-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002533115-A/3
            PD   08-OCT-2002
            PF   30-DEC-1999 JP 2000591171
            PR   31-DEC-1998 US    60/114577
            PI   THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD  PI
            JUEPPNER
            PC   C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC
              A61P19/10,
            PC   A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
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ORIGIN

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  Matches   54;  Conservative   21;  Mismatches   18;  Indels    0;  Gaps    0;

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              ||:|:::|||||:|              ||:||:||:||:||:      :|||:||||||:
Db          1 GCTGTTTCCGAAATCGGTGGTGGTGGTGGTGGTGGTGGTGGTCTGAACTCCATGGAACGT 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |::|||:|||:|||:||||||||:||||||||::
Db         61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 4
AR269042
LOCUS       AR269042                 258 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6500647.
ACCESSION   AR269042
VERSION     AR269042.1  GI:29699873
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 258)
  AUTHORS   Jung,E.-K., Park,D.-H. and Chung,S.-I.
  TITLE     Recombinant expression vector of human parathyroid hormone
  JOURNAL   Patent: US 6500647-A 26 31-DEC-2002;
            Mogam Biotechnology Research Institute; Kyonggi-Do;
            KRX;
FEATURES              Location/Qualifiers
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ORIGIN

  Query Match             61.1%;  Score 56.8;  DB 6;  Length 258;
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  Matches   50;  Conservative   20;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||: |:|||       ||:     :      :| |:|||||:|
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Db          2 CTGTTTCGGAAATCCAGCTTATGCATAACCTGGGTAAACATCTGAACTCGATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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RESULT 5
AR005132
LOCUS       AR005132                 141 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5747453.
ACCESSION   AR005132
VERSION     AR005132.1  GI:3966011
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 5747453-A 3 05-MAY-1998;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:            :|| : || ||:|
Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 6
AR005133/c
LOCUS       AR005133                 141 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5747453.
ACCESSION   AR005133
VERSION     AR005133.1  GI:3966012
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 5747453-A 5 05-MAY-1998;
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   56.0%;  Pred. No. 1.9e-05;
  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:            :|| : || ||:|
Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 7
AR177779
LOCUS       AR177779                 141 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 3 from patent US 6313092.
ACCESSION   AR177779
VERSION     AR177779.1  GI:17920134
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 6313092-A 3 06-NOV-2001;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             58.3%;  Score 54.2;  DB 6;  Length 141;
  Best Local Similarity   56.0%;  Pred. No. 1.9e-05;
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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 8
AR177780/c
LOCUS       AR177780                 141 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 5 from patent US 6313092.
ACCESSION   AR177780
VERSION     AR177780.1  GI:17920135
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 6313092-A 5 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             58.3%;  Score 54.2;  DB 6;  Length 141;
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  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 9
AR043797
LOCUS       AR043797                 207 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5814603.
ACCESSION   AR043797
VERSION     AR043797.1  GI:5964805
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 207)
  AUTHORS   Oldenburg,K.R. and Selick,H.E.
  TITLE     Compounds with PTH activity
  JOURNAL   Patent: US 5814603-A 8 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .207
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             58.3%;  Score 54.2;  DB 6;  Length 207;
  Best Local Similarity   56.0%;  Pred. No. 1.9e-05;
  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db         71 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 130

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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Db        131 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 161


RESULT 10
A36847
LOCUS       A36847                  717 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 1 from Patent WO9402510.
ACCESSION   A36847
VERSION     A36847.1  GI:2294105
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Bauer,W., Breckenridge,R., Cardinaux,F., Gombert,F., Gram,H.,
            Ramage,P., Schneider,H., Waelchli,R., Albert, Rainer and Lewis,I.
  TITLE     ANALOGS OF PTH
  JOURNAL   Patent: WO 9402510-A 1 03-FEB-1994;
            SANDOZ AG (AT)
COMMENT     Other publication HU 70459 951030
            Other publication CZ 9500088 951018
            Other publication AU 4156693 940120
            Other publication SK 4395 950607
            Other publication NZ 248137 951221
            Other publication GB 2269176 940202
            Other publication JP 6184198 940705
            Other publication CA 2100423 940116
            Other publication CN 1099801 950308
            Other publication DE 4393381T 950427
            Other publication NO 950123 950315
            Other publication ZA 9305126 950116
            Other publication FI 950171 950313.
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
     CDS             101. .562
                     /note="unnamed protein product"
                     /codon_start=1
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                     /db_xref="GI:2294106"
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ORIGIN

  Query Match             54.8%;  Score 51;  DB 6;  Length 717;
  Best Local Similarity   52.7%;  Pred. No. 0.00017;
  Matches   48;  Conservative   18;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              | |: :| ||||: || |: |:|||   :   ||:     :     ::| |:|||||:|
Db        447 CCGTATCAGAAATACAACTAATGCATAATCTGGGTAAACATCTGAATTCAATGGAACGTG 506

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|||||||:|||||| |:
Db        507 TAGAATGGCTGCGTAAAAAACTGCAGGATGT 537


RESULT 11
A36849
LOCUS       A36849                  945 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 3 from Patent WO9402510.
ACCESSION   A36849
VERSION     A36849.1  GI:2294107
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   Bauer,W., Breckenridge,R., Cardinaux,F., Gombert,F., Gram,H.,
            Ramage,P., Schneider,H., Waelchli,R., Albert, Rainer and Lewis,I.
  TITLE     ANALOGS OF PTH
  JOURNAL   Patent: WO 9402510-A 3 03-FEB-1994;
            SANDOZ AG (AT)
COMMENT     Other publication HU 70459 951030
            Other publication CZ 9500088 951018
            Other publication AU 4156693 940120
            Other publication SK 4395 950607
            Other publication NZ 248137 951221
            Other publication GB 2269176 940202
            Other publication JP 6184198 940705
            Other publication CA 2100423 940116
            Other publication CN 1099801 950308
            Other publication DE 4393381T 950427
            Other publication NO 950123 950315
            Other publication ZA 9305126 950116
            Other publication FI 950171 950313.
FEATURES             Location/Qualifiers
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                     FNAFVQRIKKERKEVAKKYSYFVHNVYDSRDDDMVALVDETFIQDIYDKMTHYEESTY
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                     LQDVHNFVALG"
ORIGIN

  Query Match             54.8%;  Score 51;  DB 6;  Length 945;
  Best Local Similarity   52.7%;  Pred. No. 0.00016;
  Matches   48;  Conservative   18;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db        675 CCGTATCAGAAATACAACTAATGCATAATCTGGGTAAACATCTGAATTCAATGGAACGTG 734

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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Db        735 TAGAATGGCTGCGTAAAAAACTGCAGGATGT 765


RESULT 12
BD234383
LOCUS       BD234383                405 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
```

```
ACCESSION   BD234383
VERSION     BD234383.1  GI:33044153
KEYWORDS    JP 2002533072-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 4 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/4
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: PCpB-RVR-hPTH fusion FH
            Key             Location/Qualifiers
            FT   CDS             (4). .(393).
FEATURES            Location/Qualifiers
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ORIGIN

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Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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RESULT 13
BD234385
LOCUS       BD234385                408 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234385
VERSION     BD234385.1  GI:33044155
KEYWORDS    JP 2002533072-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 6 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/6
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: PCpB-IEGR-hPTH fusion FH
            Key             Location/Qualifiers
            FT   CDS             (4). .(396).
FEATURES            Location/Qualifiers
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                    /organism="synthetic construct"
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  Query Match             54.2%;  Score 50.4;  DB 6;  Length 408;
  Best Local Similarity   52.2%;  Pred. No. 0.00025;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db        296 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 355

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              : |||:|||:|||:|| || |:|||||| |::
Db        356 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 387


RESULT 14
BD234386
LOCUS       BD234386                408 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234386
VERSION     BD234386.1  GI:33044156
KEYWORDS    JP 2002533072-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 7 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/7
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
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            Key             Location/Qualifiers
            FT   CDS             (4). .(396).
FEATURES            Location/Qualifiers
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ORIGIN

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  Best Local Similarity   52.2%;  Pred. No. 0.00025;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db        296 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 355

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              : |||:|||:|||:|| || |:|||||| |::
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RESULT 15
BD234384
LOCUS       BD234384                411 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234384
VERSION     BD234384.1  GI:33044154
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KEYWORDS    JP 2002533072-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 5 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/5
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: PCpB-ALY-hPTH fusion FH
            Key             Location/Qualifiers
            FT   CDS             (4). .(399).
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   52.2%;  Pred. No. 0.00025;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

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Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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GenCore version 5.1.6

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Maximum Match 100%
Listing first 45 summaries

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10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	9	38.2	41.1	450	8	W56235	W56235 zc01e11.r1
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c	21	37.2	40.0	780	1	AI028087	AI028087 ow51a12.x
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c	24	36.6	39.4	705	1	AI031553	AI031553 ow48c08.x
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	39	35	37.6	451	8	DN347334	DN347334 LIB3578-0
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ALIGNMENTS

RESULT 1
T29548
LOCUS T29548 339 bp mRNA linear EST 06-SEP-1995
DEFINITION EST83988 Human Parathyroid gland Homo sapiens cDNA 5' end similar to parathyroid hormone (HT:2194), mRNA sequence.
ACCESSION T29548
VERSION T29548.1 GI:611646
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 339)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
PUBMED 7566098
COMMENT Other_ESTs: THC23168
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)

```
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .339
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="ATCC (inhost):106648"
                      /db_xref="taxon:9606"
                      /clone_lib="Human Parathyroid gland"
                      /note="Organ: parathyroid gland"
ORIGIN

  Query Match             43.0%;  Score 40;  DB 8;  Length 339;
  Best Local Similarity   48.4%;  Pred. No. 0.12;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :      :| |:|||  | |
Db        166 CTGTGAGTGAAATACAGCTTATGCATAACCTNGGAAAACATCTNANCTCGATGGAGAGAG 225

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        226 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 256


RESULT 2
AA372113
LOCUS       AA372113                316 bp    mRNA    linear   EST 21-APR-1997
DEFINITION  EST83976 Parathyroid gland tumor II Homo sapiens cDNA 5' end
            similar to parathyroid hormone, mRNA sequence.
ACCESSION   AA372113
VERSION     AA372113.1  GI:2024432
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 316)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
   PUBMED   7566098
COMMENT     Other_ESTs: THC179155
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .316
                      /organism="Homo sapiens".
                      /mol_type="mRNA"
                      /db_xref="ATCC (inhost):176463"
                      /db_xref="taxon:9606"
                      /dev_stage="adult"
                      /clone_lib="Parathyroid gland tumor II"
                      /note="Organ: parathyroid gland; Vector: pBluescript SK-;
                      Site_1: EcoRI; Site_2: XhoI"
ORIGIN

  Query Match             41.7%;  Score 38.8;  DB 1;  Length 316;
  Best Local Similarity   48.4%;  Pred. No. 0.29;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :      :| |:|||  | |
Db        175 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGANCTCGATGGAGAGAG 234

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        235 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 265


RESULT 3
W19763
LOCUS       W19763                  324 bp    mRNA    linear   EST 03-MAY-1996
DEFINITION  zb39c01.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:305952 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W19763
VERSION     W19763.1  GI:1295880
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET
            High quality sequence stop: 222.
FEATURES              Location/Qualifiers
     source           1. .324
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="GDB:1249362"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:305952"
                      /tissue_type="parathyroid tumor"
                      /dev_stage="adult"
                      /lab_host="DH10B (ampicillin resistant)"
                      /clone_lib="Soares_parathyroid_tumor_NbHPA"
                      /note="Organ: parathyroid gland; Vector: pT7T3D
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                      oligo(dT) primer
                      [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTT
                      TTTTT-3'], double-stranded cDNA was size selected, ligated
                      to Eco RI adapters (Pharmacia), digested with Not I and
```

cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.7%;  Score 38.8;  DB 8;  Length 324;
  Best Local Similarity   48.4%;  Pred. No. 0.29;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :      :| |:|||  | |
Db         60 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 119

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        120 TAGAATGGCTGCGTAAGAANCTGCAGGATGT 150
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RESULT 4
W39062
LOCUS W39062 352 bp mRNA linear EST 15-MAY-1996
DEFINITION zb34c06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305482 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W39062
VERSION W39062.1 GI:1320771
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 352)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 286.

FEATURES Location/Qualifiers
source 1. .352
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248892"
/db_xref="taxon:9606"
/clone="IMAGE:305482"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 8;  Length 352;
  Best Local Similarity   48.4%;  Pred. No. 0.45;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :      :| |:|||  | |
Db        185 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 244

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        245 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 275
```

RESULT 5
W38966
LOCUS W38966 376 bp mRNA linear EST 15-MAY-1996
DEFINITION zb28b12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304895 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W38966
VERSION W38966.1 GI:1320674
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 376)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET.

FEATURES Location/Qualifiers
source 1. .376
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248305"
/db_xref="taxon:9606"
/clone="IMAGE:304895"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 8;  Length 376;
  Best Local Similarity   48.4%;  Pred. No. 0.45;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :      :| |:|||  | |
Db        172 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 231

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        232 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 262
```

RESULT 6
W37708
LOCUS W37708 411 bp mRNA linear EST 10-OCT-1996
DEFINITION zc10d12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321911 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W37708
VERSION W37708.1 GI:1319302
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 876 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 396.

FEATURES Location/Qualifiers
source 1. .411
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1259569"
/db_xref="taxon:9606"
/clone="IMAGE:321911"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 8;  Length 411;
  Best Local Similarity   48.4%;  Pred. No. 0.45;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :      :| |:|||  | |
Db        210 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 269

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        270 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 300
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RESULT 7
W31998
LOCUS W31998 416 bp mRNA linear EST 20-AUG-1996
DEFINITION zb96d06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:320651 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W31998
VERSION W31998.1 GI:1313010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 416)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 771 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 386.

FEATURES Location/Qualifiers
source 1. .416
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258309"
/db_xref="taxon:9606"
/clone="IMAGE:320651"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 8;  Length 416;
  Best Local Similarity   48.4%;  Pred. No. 0.46;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :      :| |:|||  | |
Db         34 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 93

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db         94 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 124
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RESULT 8
W38764
LOCUS W38764 434 bp mRNA linear EST 15-MAY-1996
DEFINITION zb27a07.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304788 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W38764
VERSION W38764.1 GI:1320471
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 253.

FEATURES Location/Qualifiers
source 1. .434
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248198"
/db_xref="taxon:9606"
/clone="IMAGE:304788"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 8;  Length 434;
  Best Local Similarity   48.4%;  Pred. No. 0.46;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :      :| |:|||  | |
Db        174 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 233

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        234 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 264
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RESULT 9
W56235
LOCUS W56235 450 bp mRNA linear EST 10-OCT-1996
DEFINITION zc01e11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321068 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W56235
VERSION W56235.1 GI:1358124
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 450)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 865 Std Error: 0.00
Seq primer: mob.REGA+ET.

FEATURES Location/Qualifiers
source 1. .450
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258726"
/db_xref="taxon:9606"
/clone="IMAGE:321068"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 41.1%; Score 38.2; DB 8; Length 450;
Best Local Similarity 48.4%; Pred. No. 0.46;
Matches 44; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :      :| |:|||  | |
Db        189 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 248

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:||||| |:
Db        249 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 279
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RESULT 10
W33077
LOCUS W33077 453 bp mRNA linear EST 10-OCT-1996
DEFINITION zc07a12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321598 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W33077
VERSION W33077.1 GI:1315062
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 453)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 871 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 367.
FEATURES Location/Qualifiers
source 1. .453
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1259256"
/db_xref="taxon:9606"
/clone="IMAGE:321598"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 41.1%; Score 38.2; DB 8; Length 453;
Best Local Similarity 48.4%; Pred. No. 0.46;
Matches 44; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :      :| |:|||  | |
Db        201 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 260

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:||||| |:
Db        261 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 291
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RESULT 11
W56820
LOCUS W56820 496 bp mRNA linear EST 10-OCT-1996
DEFINITION zc01a03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321004 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W56820
VERSION W56820.1 GI:1358743
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 496)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 858 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 424.
FEATURES Location/Qualifiers
source 1. .496
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258662"
/db_xref="taxon:9606"
/clone="IMAGE:321004"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 8;  Length 496;
  Best Local Similarity   48.4%;  Pred. No. 0.47;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :      :| |:|||  | |
Db        179 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 238

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        239 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 269
```

RESULT 12
W19765
LOCUS W19765 536 bp mRNA linear EST 03-MAY-1996
DEFINITION zb39c03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305956 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W19765
VERSION W19765.1 GI:1295882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 536)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 352.
FEATURES Location/Qualifiers
source 1. .536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249366"
/db_xref="taxon:9606"
/clone="IMAGE:305956"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 8;  Length 536;
  Best Local Similarity   48.4%;  Pred. No. 0.47;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||       :      :| |:|||  | |
Db        189 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 248

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        249 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 279
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RESULT 13
W56120
LOCUS W56120 576 bp mRNA linear EST 11-OCT-1996
DEFINITION zc56h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326363 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W56120
VERSION W56120.1 GI:1358009
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 576)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 904 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 433.
FEATURES Location/Qualifiers
source 1. .576
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1260565"
/db_xref="taxon:9606"
/clone="IMAGE:326363"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 8;  Length 576;
  Best Local Similarity   48.4%;  Pred. No. 0.47;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :      :| |:|||  | |
Db        184 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 243

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        244 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 274
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RESULT 14
W39202
LOCUS W39202 583 bp mRNA linear EST 15-MAY-1996
DEFINITION zb35h03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305621 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W39202
VERSION W39202.1 GI:1320911
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 400.
FEATURES Location/Qualifiers
source 1. .583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249031"
/db_xref="taxon:9606"
/clone="IMAGE:305621"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 8;  Length 583;
  Best Local Similarity   48.4%;  Pred. No. 0.48;
  Matches   44;  Conservative   14;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:    ||||: ||||: |:|||       ||      :      :| |:|||  | |
Db         53 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 112

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| || |:|||||| |:
Db        113 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 143
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RESULT 15
BH958789/c
LOCUS BH958789 702 bp DNA linear GSS 01-OCT-2002
DEFINITION odj08c01.b1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
ACCESSION BH958789
VERSION BH958789.1 GI:23440016
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 702)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odj08 row: c column: 01
Seq primer: -21UPpOT forward
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 551.
FEATURES Location/Qualifiers
source 1. .702
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

```
  Query Match             41.1%;  Score 38.2;  DB 9;  Length 702;
  Best Local Similarity   49.3%;  Pred. No. 0.49;
  Matches   37;  Conservative   15;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          7 UCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAA 66
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Qy         67 UGGCUGCGUAAAAAA 81
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Db        606 GACATTGATACAAGA 592
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Search completed: November 24, 2005, 01:30:29
Job time : 1824 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:44:43 ; Search time 73.6667 Seconds
(without alignments)
2244.071 Million cell updates/sec

Title: US-09-475-158A-15
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	56.8	61.1	258	3	US-09-463-282D-26	Sequence 26, Appl
	2	54.2	58.3	141	2	US-08-468-275-3	Sequence 3, Appli
c	3	54.2	58.3	141	2	US-08-468-275-5	Sequence 5, Appli
	4	54.2	58.3	141	3	US-09-007-466-3	Sequence 3, Appli
c	5	54.2	58.3	141	3	US-09-007-466-5	Sequence 5, Appli
	6	54.2	58.3	141	3	US-08-952-980B-3	Sequence 3, Appli
c	7	54.2	58.3	141	3	US-08-952-980B-5	Sequence 5, Appli
	8	54.2	58.3	207	2	US-08-142-551B-8	Sequence 8, Appli
	9	46.2	49.7	252	2	US-08-733-446-58	Sequence 58, Appl
	10	44.6	48.0	102	3	US-10-340-484-14	Sequence 14, Appl
	11	44.6	48.0	252	2	US-08-689-190-1	Sequence 1, Appli
	12	44.6	48.0	252	2	US-08-733-446-23	Sequence 23, Appl
	13	44.6	48.0	252	2	US-08-733-446-56	Sequence 56, Appl
	14	44.6	48.0	252	2	US-08-835-231-34	Sequence 34, Appl
	15	44.6	48.0	252	3	US-09-108-661-34	Sequence 34, Appl
	16	44.6	48.0	263	2	US-08-689-190-3	Sequence 3, Appli
	17	44.6	48.0	263	2	US-08-733-446-32	Sequence 32, Appl
c	18	44.6	48.0	265	2	US-08-689-190-4	Sequence 4, Appli
c	19	44.6	48.0	265	2	US-08-733-446-33	Sequence 33, Appl
c	20	43.4	46.7	74	2	US-08-142-551B-132	Sequence 132, App
	21	43	46.2	67	3	US-09-068-738A-9	Sequence 9, Appli
	22	43	46.2	252	2	US-08-733-446-62	Sequence 62, Appl
	23	41.4	44.5	252	2	US-08-733-446-57	Sequence 57, Appl
	24	38.2	41.1	243	2	US-08-733-446-22	Sequence 22, Appl
	25	38.2	41.1	252	2	US-07-863-014-1	Sequence 1, Appli
	26	38.2	41.1	252	2	US-08-332-453-1	Sequence 1, Appli
	27	38.2	41.1	254	2	US-08-733-446-30	Sequence 30, Appl
c	28	38.2	41.1	256	2	US-08-733-446-31	Sequence 31, Appl
	29	38.2	41.1	537	2	US-08-835-231-5	Sequence 5, Appli
	30	38.2	41.1	537	2	US-08-835-231-6	Sequence 6, Appli
	31	38.2	41.1	537	3	US-09-108-661-5	Sequence 5, Appli
	32	38.2	41.1	537	3	US-09-108-661-6	Sequence 6, Appli
c	33	38.2	41.1	601	3	US-09-949-016-18519	Sequence 18519, A
c	34	38.2	41.1	601	3	US-09-949-016-66782	Sequence 66782, A
	35	38.2	41.1	772	3	US-09-949-016-51	Sequence 51, Appl
	36	38.2	41.1	773	3	US-09-949-016-1970	Sequence 1970, Ap
	37	38.2	41.1	7926	3	US-09-949-016-11793	Sequence 11793, A
	38	38.2	41.1	7926	3	US-09-949-016-13712	Sequence 13712, A
c	39	37.4	40.2	67	3	US-09-068-738A-10	Sequence 10, Appl
	40	36.8	39.6	240	2	US-08-733-446-21	Sequence 21, Appl
	41	36.8	39.6	248	2	US-08-733-446-26	Sequence 26, Appl
	42	36.8	39.6	251	2	US-08-733-446-28	Sequence 28, Appl
c	43	36.8	39.6	253	2	US-08-733-446-29	Sequence 29, Appl
	44	36.4	39.1	45	3	US-09-463-282D-5	Sequence 5, Appli
c	45	35.8	38.5	250	2	US-08-733-446-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-463-282D-26
; Sequence 26, Application US/09463282D
; Patent No. 6500647
; GENERAL INFORMATION:
; APPLICANT: Jung, Eun-Kyung
; APPLICANT: Park, Doo-Hong
; APPLICANT: Chung, Soo Il
; TITLE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE
; FILE REFERENCE: 0136/0G626
; CURRENT APPLICATION NUMBER: US/09/463,282D
; CURRENT FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: PCT/KR98/00146
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: KR 1997-35230
; PRIOR FILING DATE: 1997-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-463-282D-26

Query Match 61.1%; Score 56.8; DB 3; Length 258;
Best Local Similarity 54.3%; Pred. No. 3.3e-09;
Matches 50; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

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Db          2 CTGTTTCGGAAATCCAGCTTATGCATAACCTGGGTAAACATCTGAACTCGATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGATGTT 93
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RESULT 2
US-08-468-275-3
; Sequence 3, Application US/08468275
; Patent No. 5747453
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 10

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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,275
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..138
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  25
US-08-468-275-3

  Query Match             58.3%;  Score 54.2;  DB 2;  Length 141;
  Best Local Similarity   56.0%;  Pred. No. 1.9e-08;
  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 3
US-08-468-275-5/c
; Sequence 5, Application US/08468275
; Patent No. 5747453
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,275
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-468-275-5

  Query Match             58.3%;  Score 54.2;  DB 2;  Length 141;
  Best Local Similarity   56.0%;  Pred. No. 1.9e-08;
  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:            :|| : || ||:|
Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 4
US-09-007-466-3
; Sequence 3, Application US/09007466
; Patent No. 6313092
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/007,466
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/468,275
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..138
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  25
US-09-007-466-3

  Query Match             58.3%;  Score 54.2;  DB 3;  Length 141;
  Best Local Similarity   56.0%;  Pred. No. 1.9e-08;
  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
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Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 5
US-09-007-466-5/c
; Sequence 5, Application US/09007466
; Patent No. 6313092
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/007,466
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/468,275
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  0360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-007-466-5

  Query Match             58.3%;  Score 54.2;  DB 3;  Length 141;
  Best Local Similarity   56.0%;  Pred. No. 1.9e-08;
  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

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Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 6
US-08-952-980B-3
; Sequence 3, Application US/08952980B
; Patent No. 6333189
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/952,980B
;      FILING DATE:  20-NOV-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  2349 CIP 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 496-8150
;      TELEFAX:  (650) 496-8048
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..138
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  25
US-08-952-980B-3

  Query Match             58.3%;  Score 54.2;  DB 3;  Length 141;
  Best Local Similarity   56.0%;  Pred. No. 1.9e-08;
  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
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Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 7
US-08-952-980B-5/c
; Sequence 5, Application US/08952980B
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; Patent No. 6333189
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/952,980B
;      FILING DATE:  20-NOV-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  2349 CIP 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 496-8150
;      TELEFAX:  (650) 496-8048
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-952-980B-5

  Query Match             58.3%;  Score 54.2;  DB 3;  Length 141;
  Best Local Similarity   56.0%;  Pred. No. 1.9e-08;
  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
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Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 8
US-08-142-551B-8
; Sequence 8, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  207 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..201
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..51
;      OTHER INFORMATION:  /note= "Encodes the leader peptide
;      OTHER INFORMATION:  sequence that serves to direct the protein into
;      OTHER INFORMATION:  inclusion bodies."
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  70..174
;      OTHER INFORMATION:  /note= "Encodes the protein or
;      OTHER INFORMATION:  peptide of interest"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  175..207
;      OTHER INFORMATION:  /note= "Encodes amino acid sequence
;      OTHER INFORMATION:  having six histamines that serves as a tag for the
;      OTHER INFORMATION:  purification of the protein on a nickel column."
US-08-142-551B-8

  Query Match             58.3%;  Score 54.2;  DB 2;  Length 207;
  Best Local Similarity   56.0%;  Pred. No. 2.2e-08;
  Matches   51;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              | |:::||||||:|||||:| :||||      ||:            :|| : || ||:|
Db        71 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 130

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db        131 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 161


RESULT 9
US-08-733-446-58
; Sequence 58, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..252
;      NAME/KEY:  mutation
;      LOCATION:  19...24
;      IDENTIFICATION METHOD:  E
US-08-733-446-58

  Query Match             49.7%;  Score 46.2;  DB 2;  Length 252;
  Best Local Similarity   50.5%;  Pred. No. 9.7e-06;
  Matches   46;  Conservative   17;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|: :|||| |: ||||:| :|||      :||      :      :|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGCTGCTGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 10
US-10-340-484-14
; Sequence 14, Application US/10340484
; Patent No. 6875739
; GENERAL INFORMATION:
;  APPLICANT: Stewart, Andrew F.
;  TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
;  TITLE OF INVENTION:  Drugs
;  FILE REFERENCE: 25200-501
;  CURRENT APPLICATION NUMBER: US/10/340,484
;  CURRENT FILING DATE:  2003-01-10
;  PRIOR APPLICATION NUMBER: 60/347,215
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: 60/353,296
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: 60/368,955
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: 60/379,125
;  PRIOR FILING DATE: 2002-05-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 102
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-340-484-14

  Query Match             48.0%;  Score 44.6;  DB 3;  Length 102;
  Best Local Similarity   49.5%;  Pred. No. 2.5e-05;
  Matches   45;  Conservative   17;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      :      :|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 11
US-08-689-190-1
; Sequence 1, Application US/08689190
; Patent No. 5714349
; GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    APPLICANT:  OSHIKA, Yuri
;    APPLICANT:  YAMADA, Takao
;    TITLE OF INVENTION:  SYNTHETIC GENE CODING FOR HUMAN
;    TITLE OF INVENTION:  PARATHYROID HORMONE
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/689,190
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/006,197
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/016,171
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/765,371
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILLIAMS, Gregory D
;      REGISTRATION NUMBER:  30,901
;      REFERENCE/DOCKET NUMBER:  41,288
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthesizing DNA
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;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..252
;       IDENTIFICATION METHOD:  E
;     FEATURE:
;       NAME/KEY:  MUTATION
;       LOCATION:  7, 8, 9, 12, 15, 19, 21, 33, 36, 43, 51, 58, 60,
;       IDENTIFICATION METHOD:  S
US-08-689-190-1

  Query Match             48.0%;  Score 44.6;  DB 2;  Length 252;
  Best Local Similarity   49.5%;  Pred. No. 3.2e-05;
  Matches   45;  Conservative   17;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      :      :|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 12
US-08-733-446-23
; Sequence 23, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid,  synthetic DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..252
;      IDENTIFICATION METHOD:  E
US-08-733-446-23

  Query Match             48.0%;  Score 44.6;  DB 2;  Length 252;
  Best Local Similarity   49.5%;  Pred. No. 3.2e-05;
  Matches   45;  Conservative   17;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      :      :|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 13
US-08-733-446-56
; Sequence 56, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..252
;      NAME/KEY:  mutation
;      LOCATION:  103...105
;      IDENTIFICATION METHOD:  E
US-08-733-446-56

  Query Match             48.0%;  Score 44.6;  DB 2;  Length 252;
  Best Local Similarity   49.5%;  Pred. No. 3.2e-05;
  Matches   45;  Conservative   17;  Mismatches   29;  Indels    0;  Gaps    0;
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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      :      :|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 14
US-08-835-231-34
; Sequence 34, Application US/08835231
; Patent No. 5861284
;  GENERAL INFORMATION:
;    APPLICANT:  NISHIMURA, Osamu
;    APPLICANT:  KURIYAMA, Masato
;    APPLICANT:  KOYAMA, No. 5861284uyuki
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  METHOD FOR PRODUCING A BIOLOGICALLY
;    TITLE OF INVENTION:  ACTIVE RECOMBINANT CYSTEINE-FREE
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/835,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,709
;      FILING DATE:  07-DEC-1994
;      APPLICATION NUMBER:  07/838,857
;      FILING DATE:  18-FEB-1992
;      APPLICATION NUMBER:  JP 024841
;      FILING DATE:  19-FEB-1991
;      APPLICATION NUMBER:  JP 0271438
;      FILING DATE:  18-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  41614-FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Synthetic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Synthetic DNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...252
US-08-835-231-34

  Query Match             48.0%;  Score 44.6;  DB 2;  Length 252;
  Best Local Similarity   49.5%;  Pred. No. 3.2e-05;
  Matches   45;  Conservative   17;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      :      :|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 15
US-09-108-661-34
; Sequence 34, Application US/09108661
; Patent No. 6287806
;  GENERAL INFORMATION:
;    APPLICANT:  NISHIMURA, Osamu
;    APPLICANT:  KURIYAMA, Masato
;    APPLICANT:  KOYAMA, No. 6287806uyuki
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  METHOD FOR PRODUCING A BIOLOGICALLY
;    TITLE OF INVENTION:  ACTIVE RECOMBINANT CYSTEINE-FREE
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/108,661
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,709
;      FILING DATE:  07-DEC-1994
;      APPLICATION NUMBER:  07/838,857
;      FILING DATE:  18-FEB-1992
;      APPLICATION NUMBER:  JP 024841
;      FILING DATE:  19-FEB-1991
;      APPLICATION NUMBER:  JP 0271438
;      FILING DATE:  18-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  41614-FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Synthetic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Synthetic DNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...252
US-09-108-661-34
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Query Match 48.0%; Score 44.6; DB 3; Length 252;
Best Local Similarity 49.5%; Pred. No. 3.2e-05;
Matches 45; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|: :|||| |: ||| : |:|||      :||      :      :|||:||| ||:|
Db          2 CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|| ||  :|||||| |:
Db         62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92
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Search completed: November 24, 2005, 01:34:14
Job time : 73.6667 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 23:59:22 ; Search time 412.667 Seconds
(without alignments)
1863.616 Million cell updates/sec

Title: US-09-475-158A-15
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	64.5	102	9	US-10-997-078-60	Sequence 60, Appl
2	60	64.5	102	9	US-10-997-700-33	Sequence 33, Appl
3	60	64.5	111	9	US-10-997-078-61	Sequence 61, Appl
4	60	64.5	111	9	US-10-997-700-34	Sequence 34, Appl
5	60	64.5	117	9	US-10-997-078-141	Sequence 141, App
6	60	64.5	252	9	US-10-997-078-62	Sequence 62, Appl
7	60	64.5	252	9	US-10-997-700-35	Sequence 35, Appl
8	60	64.5	264	9	US-10-997-700-89	Sequence 89, Appl
9	60	64.5	276	9	US-10-997-762-18	Sequence 18, Appl
10	60	64.5	276	9	US-10-997-822-3	Sequence 3, Appli
11	60	64.5	276	9	US-10-997-700-75	Sequence 75, Appl
12	60	64.5	282	9	US-10-997-078-133	Sequence 133, App
13	60	64.5	291	9	US-10-997-700-76	Sequence 76, Appl
14	60	64.5	291	9	US-10-997-700-77	Sequence 77, Appl
15	60	64.5	321	9	US-10-997-700-91	Sequence 91, Appl
16	60	64.5	420	9	US-10-997-700-93	Sequence 93, Appl
17	60	64.5	426	9	US-10-997-762-20	Sequence 20, Appl
18	58.4	62.8	489	6	US-10-117-109-14	Sequence 14, Appl
19	58.4	62.8	489	6	US-10-407-078-14	Sequence 14, Appl
20	58.4	62.8	489	6	US-10-407-078-43	Sequence 43, Appl
21	51	54.8	717	8	US-10-848-279-7	Sequence 7, Appli
22	51	54.8	945	8	US-10-848-279-8	Sequence 8, Appli
23	47.6	51.2	348	6	US-10-437-038-1	Sequence 1, Appli
24	47.6	51.2	348	6	US-10-359-091-1	Sequence 1, Appli
25	47.6	51.2	432	6	US-10-437-038-3	Sequence 3, Appli
26	47.6	51.2	432	6	US-10-359-091-3	Sequence 3, Appli
27	47.6	51.2	874	6	US-10-437-038-7	Sequence 7, Appli
28	47.6	51.2	874	6	US-10-359-091-7	Sequence 7, Appli
29	44.6	48.0	102	6	US-10-340-484-14	Sequence 14, Appl
30	44.2	47.5	106	3	US-09-746-945-11	Sequence 11, Appl
c 31	44.2	47.5	107	3	US-09-746-945-12	Sequence 12, Appl
32	43	46.2	258	8	US-10-343-189-15	Sequence 15, Appl
33	40.8	43.9	252	7	US-10-398-449-2	Sequence 2, Appli
34	39	41.9	51	3	US-09-879-257A-51	Sequence 51, Appl
c 35	39	41.9	51	3	US-09-879-257A-52	Sequence 52, Appl
36	38.2	41.1	102	9	US-10-775-204-24	Sequence 24, Appl
37	38.2	41.1	102	9	US-10-775-204-25	Sequence 25, Appl
38	38.2	41.1	102	9	US-10-775-204-51	Sequence 51, Appl
39	38.2	41.1	102	9	US-10-775-204-52	Sequence 52, Appl
40	38.2	41.1	102	9	US-10-775-204-57	Sequence 57, Appl
41	38.2	41.1	102	9	US-10-775-204-60	Sequence 60, Appl
42	38.2	41.1	102	9	US-10-775-204-61	Sequence 61, Appl
43	38.2	41.1	102	9	US-10-775-204-64	Sequence 64, Appl
44	38.2	41.1	102	9	US-10-775-204-69	Sequence 69, Appl
45	38.2	41.1	102	9	US-10-775-204-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-10-997-078-60
; Sequence 60, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
; APPLICANT: Restoragen, Inc.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
; FILE REFERENCE: 1627.010US1
; CURRENT APPLICATION NUMBER: US/10/997,078
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16643
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,370
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PTH(1-34).
US-10-997-078-60

Query Match 64.5%; Score 60; DB 9; Length 102;
Best Local Similarity 57.6%; Pred. No. 6.5e-11;
Matches 53; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

```
Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:           :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
```

RESULT 2
US-10-997-700-33
; Sequence 33, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:

```
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 102
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-34).
US-10-997-700-33

  Query Match             64.5%;  Score 60;  DB 9;  Length 102;
  Best Local Similarity   57.6%;  Pred. No. 6.5e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:           :| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 3
US-10-997-078-61
; Sequence 61, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 111
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-37).
US-10-997-078-61

  Query Match             64.5%;  Score 60;  DB 9;  Length 111;
  Best Local Similarity   57.6%;  Pred. No. 6.6e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| |||:|||||:||:||||      ||:           :| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 4
US-10-997-700-34
; Sequence 34, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 111
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-37).
US-10-997-700-34

  Query Match             64.5%;  Score 60;  DB 9;  Length 111;
  Best Local Similarity   57.6%;  Pred. No. 6.6e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:           :| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 5
US-10-997-078-141
; Sequence 141, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
;   LENGTH: 117
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PTH sequence.
US-10-997-078-141

  Query Match             64.5%;  Score 60;  DB 9;  Length 117;
  Best Local Similarity   57.6%;  Pred. No. 6.7e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:           :| |:|||||:|
```

```
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 6
US-10-997-078-62
; Sequence 62, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
;   LENGTH: 252
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-84).
US-10-997-078-62

  Query Match             64.5%;  Score 60;  DB 9;  Length 252;
  Best Local Similarity   57.6%;  Pred. No. 8e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:           :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 7
US-10-997-700-35
; Sequence 35, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 252
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-84).
US-10-997-700-35

  Query Match             64.5%;  Score 60;  DB 9;  Length 252;
  Best Local Similarity   57.6%;  Pred. No. 8e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:           :| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 8
US-10-997-700-89
; Sequence 89, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
;   LENGTH: 264
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic pBN121-M-PTH(1-84).
US-10-997-700-89

  Query Match             64.5%;  Score 60;  DB 9;  Length 264;
  Best Local Similarity   57.6%;  Pred. No. 8.1e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:           :| |:||||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         65 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 96


RESULT 9
US-10-997-762-18
; Sequence 18, Application US/10997762
; Publication No. US20050227313A1
; GENERAL INFORMATION:
;  APPLICANT: Seo, Jin Seog
;  APPLICANT:  Strydom, Daniel
;  APPLICANT:  Holmquist, Barton
;  APPLICANT:  Restoragen Inc.
;  TITLE OF INVENTION: Polypeptide Cleavage Process
;  FILE REFERENCE: 1627.026US1
;  CURRENT APPLICATION NUMBER: US/10/997,762
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16468
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,488
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 276
;   TYPE: DNA
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence of a chimeric synthetic protein
US-10-997-762-18

  Query Match             64.5%;  Score 60;  DB 9;  Length 276;
  Best Local Similarity   57.6%;  Pred. No. 8.2e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:|||||:|
Db        173 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 232

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264


RESULT 10
US-10-997-822-3
; Sequence 3, Application US/10997822
; Publication No. US20050227314A1
; GENERAL INFORMATION:
;  APPLICANT: Holmquist, B.
;  APPLICANT:  Strydom, D.
;  APPLICANT:  Gensalk, X.
;  APPLICANT:  Cryer, R.
;  TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
;  FILE REFERENCE: 1627.011US1
;  CURRENT APPLICATION NUMBER: US/10/997,822
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16647
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,484
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 276
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence of a synthetic chimeric protein.
US-10-997-822-3

  Query Match             64.5%;  Score 60;  DB 9;  Length 276;
  Best Local Similarity   57.6%;  Pred. No. 8.2e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:|||||:|
Db        173 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 232

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264


RESULT 11
US-10-997-700-75
; Sequence 75, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
;   LENGTH: 276
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PCR product.
US-10-997-700-75

  Query Match             64.5%;  Score 60;  DB 9;  Length 276;
  Best Local Similarity   57.6%;  Pred. No. 8.2e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:|||||:|
Db         14 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 73

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         74 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 105


RESULT 12
US-10-997-078-133
; Sequence 133, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
;   LENGTH: 282
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic sequence for the T7tagVg-PTH(1-34) cassette.
US-10-997-078-133

  Query Match             64.5%;  Score 60;  DB 9;  Length 282;
  Best Local Similarity   57.6%;  Pred. No. 8.2e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:|||||:|
Db        167 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 226

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        227 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 258


RESULT 13
US-10-997-700-76
; Sequence 76, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
```

```
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 291
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PCR product.
US-10-997-700-76

  Query Match             64.5%;  Score 60;  DB 9;  Length 291;
  Best Local Similarity   57.6%;  Pred. No. 8.3e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db         29 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 88

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         89 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 120


RESULT 14
US-10-997-700-77
; Sequence 77, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
;   LENGTH: 291
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PCR product.
US-10-997-700-77

  Query Match             64.5%;  Score 60;  DB 9;  Length 291;
  Best Local Similarity   57.6%;  Pred. No. 8.3e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db         29 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 88

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         89 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 120


RESULT 15
US-10-997-700-91
; Sequence 91, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic pBN121-T7tag-CH-PTH(1-84).
US-10-997-700-91

  Query Match             64.5%;  Score 60;  DB 9;  Length 321;
  Best Local Similarity   57.6%;  Pred. No. 8.5e-11;
  Matches   53;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:::| ||||:|||||:||:||||      ||:            :| |:||||||:|
Db         62 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 121

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        122 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 153


Search completed: November 24, 2005, 04:46:56
Job time : 413.667 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 24, 2005, 01:30:39 ; Search time 195 Seconds
(without alignments)
70.875 Million cell updates/sec

Title: US-09-475-158A-15
Perfect score: 93
Sequence: 1 gcuguuuccgaaauccagcu.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3205263 seqs, 74304013 residues

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	28.4	30.5	2327	1	US-10-821-234-760	Sequence 760, App
	2	24.6	26.5	6497	1	US-10-821-234-839	Sequence 839, App
c	3	24.2	26.0	3138	1	US-10-392-234A-15	Sequence 15, Appl
	4	23.8	25.6	5690	1	US-10-485-517-4	Sequence 4, Appli
c	5	23.4	25.2	947	1	US-10-927-641-116	Sequence 116, App
	6	23.4	25.2	1657	1	US-10-821-234-318	Sequence 318, App
c	7	23.2	24.9	3893	1	US-10-821-234-255	Sequence 255, App
c	8	23	24.7	3507	1	US-10-509-422-1	Sequence 1, Appli
c	9	23	24.7	3704	1	US-10-509-422-3	Sequence 3, Appli
c	10	23	24.7	26323	7	US-11-005-030-1	Sequence 1, Appli
c	11	22.6	24.3	481	1	US-10-667-295-44	Sequence 44, Appl
c	12	22.6	24.3	2218	1	US-10-821-234-119	Sequence 119, App
c	13	22.6	24.3	7979	1	US-10-509-921-9	Sequence 9, Appli
c	14	22.6	24.3	7979	1	US-10-509-921-10	Sequence 10, Appl
c	15	22.6	24.3	7979	1	US-10-509-921-11	Sequence 11, Appl
c	16	22.6	24.3	7979	1	US-10-509-921-12	Sequence 12, Appl
c	17	22.6	24.3	7989	1	US-10-509-921-8	Sequence 8, Appli
c	18	22.6	24.3	14770	1	US-10-821-234-268	Sequence 268, App
	19	22.2	23.9	1984	1	US-10-502-893-1	Sequence 1, Appli
c	20	22.2	23.9	55763	1	US-10-972-766-1	Sequence 1, Appli
	21	22	23.7	409	1	US-10-839-799-28	Sequence 28, Appl
	22	22	23.7	1254	1	US-10-858-730-35	Sequence 35, Appl
	23	22	23.7	1899	1	US-10-689-742-77	Sequence 77, Appl
c	24	22	23.7	2043	1	US-10-467-962B-100	Sequence 100, App
c	25	22	23.7	2631	9	US-11-077-550-65	Sequence 65, Appl
c	26	22	23.7	2727	9	US-11-077-550-63	Sequence 63, Appl
c	27	22	23.7	2745	9	US-11-077-550-59	Sequence 59, Appl
c	28	22	23.7	2748	1	US-10-821-234-662	Sequence 662, App
c	29	22	23.7	2850	9	US-11-077-550-67	Sequence 67, Appl
c	30	22	23.7	3393	9	US-11-077-550-138	Sequence 138, App
	31	21.8	23.4	3160	8	US-11-112-944-8	Sequence 8, Appli
c	32	21.8	23.4	5796	1	US-10-821-234-62	Sequence 62, Appl
	33	21.6	23.2	809	8	US-11-132-839-6	Sequence 6, Appli
	34	21.6	23.2	1714	1	US-10-131-826A-251	Sequence 251, App
c	35	21.4	23.0	2458	1	US-10-131-826A-387	Sequence 387, App
c	36	21.4	23.0	2743	1	US-10-821-234-267	Sequence 267, App
c	37	21.4	23.0	3305	7	US-11-017-550-68	Sequence 68, Appl
c	38	21.4	23.0	3371	1	US-10-131-826A-35	Sequence 35, Appl
c	39	21.4	23.0	12391	7	US-11-017-550-67	Sequence 67, Appl
	40	21.4	23.0	12732	1	US-10-802-796-1	Sequence 1, Appli
c	41	21.2	22.8	59	7	US-11-040-159-127	Sequence 127, App
	42	21.2	22.8	1392	1	US-10-793-626-349	Sequence 349, App
c	43	21.2	22.8	3328	1	US-10-793-626-3644	Sequence 3644, Ap
	44	21.2	22.8	3701	1	US-10-793-626-3392	Sequence 3392, Ap
c	45	21.2	22.8	4035	1	US-10-793-626-3525	Sequence 3525, Ap

ALIGNMENTS

RESULT 1
US-10-821-234-760/c
; Sequence 760, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 760
; LENGTH: 2327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-760

Query Match 30.5%; Score 28.4; DB 1; Length 2327;
Best Local Similarity 44.9%; Pred. No. 0.82;
Matches 35; Conservative 12; Mismatches 31; Indels 0; Gaps 0;

```
Qy          16 CAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGU 75
               ||||:| :|| |   ||:||:|| || ||:|   |    || | :| :|   |  :  |:
Db         894 CAGCTGCTGCCCCTGGGTGGTGGAGGCGGTGACGCTGACGACCATGATGGTGGCATTGGT 835

Qy          76 AAAAAACUGCAGGACGUU 93
                  | | |:|| | | |::
Db         834 GAGGATCTGCTGCAGGTT 817
```

RESULT 2
US-10-821-234-839
; Sequence 839, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

```
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 839
;   LENGTH: 6497
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-839

  Query Match             26.5%;  Score 24.6;  DB 1;  Length 6497;
  Best Local Similarity   41.3%;  Pred. No. 18;
  Matches   26;  Conservative   13;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              | | :: |  ||  |   :  : || ||:||:||:| :||:||:||:       ||  |:|
Db       3144 CCGGTTACCCAAGGCTTGTTGTCCATGGTGGTGGTGATGGTGGTGGTGGTGATGGTG 3203

Qy         62 UUG 64
                :|
Db       3204 ATG 3206


RESULT 3
US-10-392-234A-15/c
; Sequence 15, Application US/10392234A
; Publication No. US20050255538A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia and Upjohn Corporation
;  APPLICANT:  Buxser, Steven
;  APPLICANT:  Poole, Keith
;  APPLICANT:  Decker, Douglas
;  APPLICANT:  Xiaznhi Li
;  TITLE OF INVENTION: Method for Screening for acrAB Transporter Family Inhibitors
;  FILE REFERENCE: 6206
;  CURRENT APPLICATION NUMBER: US/10/392,234A
;  CURRENT FILING DATE:  2003-03-17
;  PRIOR APPLICATION NUMBER: US 60/364,935
;  PRIOR FILING DATE: 2002-03-15
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 3138
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-10-392-234A-15

  Query Match             26.0%;  Score 24.2;  DB 1;  Length 3138;
  Best Local Similarity   50.7%;  Pred. No. 21;
  Matches   35;  Conservative    6;  Mismatches   28;  Indels    0;  Gaps    0;

Qy         23 UGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAAC 82
              :||||||  | :||  |  | || | :  |  || ||  |::||  ||| |  : |  | |
Db        137 TGCACGGCGATGGCCGGCGGGGCGATGGCCGGGTACTGGTTGACCGGCAGACTGAGGATC 78

Qy         83 UGCAGGACG 91
                ||||  ||
Db         77 GACAGGCCG 69


RESULT 4
US-10-485-517-4
; Sequence 4, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
;  APPLICANT: University of Sheffield
;  APPLICANT:  Biosynexus Incorporated
;  APPLICANT:  Foster, Simon
;  APPLICANT:  Mond, James
;  TITLE OF INVENTION: Antigenic Polypeptides
;  FILE REFERENCE: P100629WO
;  CURRENT APPLICATION NUMBER: US/10/485,517
;  CURRENT FILING DATE:  2004-02-02
;  PRIOR APPLICATION NUMBER: GB 0118825.9
;  PRIOR FILING DATE: 2001-08-02
;  PRIOR APPLICATION NUMBER: GB 0200349.9
;  PRIOR FILING DATE: 2002-01-09
;  NUMBER OF SEQ ID NOS: 424
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 5690
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-485-517-4

  Query Match             25.6%;  Score 23.8;  DB 1;  Length 5690;
  Best Local Similarity   40.3%;  Pred. No. 32;
  Matches   27;  Conservative   13;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60
              | :|:::|||      |      |      ||:|  ||:|| | :||:||  | |: | | |:
Db        520 GGTGTTTCCGGCTCGCTTGGTACTTCTGGTGTCGGTGGCGTTGGTGGCACGATTGGAGGT 579

Qy         61 GUUGAAU 67
                |::| |:
Db        580 GTTGTAT 586


RESULT 5
US-10-927-641-116/c
; Sequence 116, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
;  APPLICANT: Perera, Ranjan
;  APPLICANT:  Rice, Stephen
;  APPLICANT:  Eagleton, Clare
;  APPLICANT:  Lasham, Annette
;  APPLICANT:  Wood, Marion
;  APPLICANT:  Visser, Elizabeth
;  TITLE OF INVENTION: Compositions and Methods for the
;  TITLE OF INVENTION:  Modification of Gene Expression
;  FILE REFERENCE: 11000.1036c4
;  CURRENT APPLICATION NUMBER: US/10/927,641
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: PRIOR  APPLICATION NUMBER: US/10/137,036
;  PRIOR FILING DATE: 2002-04-30
;  PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
;  PRIOR FILING DATE: 2000-06-20
;  PRIOR APPLICATION NUMBER: PCT/NZ00/00018
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
;  PRIOR FILING DATE: 1999-07-30
;  PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
;  PRIOR FILING DATE: 1999-03-25
;  NUMBER OF SEQ ID NOS: 143
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116
;   LENGTH: 947
;   TYPE: DNA
;   ORGANISM: Eucalyptus grandis
US-10-927-641-116

  Query Match             25.2%;  Score 23.4;  DB 1;  Length 947;
  Best Local Similarity   51.2%;  Pred. No. 29;
  Matches   21;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         26 ACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAA 66
              | ||:||:||:||:||:||:||:       |    |:| :|||
Db        528 ATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGAA 488
```

```
RESULT 6
US-10-821-234-318
; Sequence 318, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 318
;   LENGTH: 1657
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-318

  Query Match             25.2%;  Score 23.4;  DB 1;  Length 1657;
  Best Local Similarity   54.4%;  Pred. No. 33;
  Matches   31;  Conservative    5;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          5 UUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              :::||||| :||| | |  || ||  || ||  | || ||:||   |  ||  || |
Db       1231 TTTCCGAAGTCCATCAGGGGCGCGCCGGCGGCAGGGGCGGTGGGCACTGGGGCCGCG 1287


RESULT 7
US-10-821-234-255/c
; Sequence 255, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 255
;   LENGTH: 3893
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-255

  Query Match             24.9%;  Score 23.2;  DB 1;  Length 3893;
  Best Local Similarity   43.2%;  Pred. No. 47;
  Matches   19;  Conservative   12;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          5 UUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGU 48
              :: | ||  :   | :| :|    |:||:||:||:||:||:||:
Db       2665 TTCCGGAGGTGATGATGGTGGTGAGTGGTGGTGGTGGTGGTGGT 2622


RESULT 8
US-10-509-422-1/c
; Sequence 1, Application US/10509422
; Publication No. US20050244825A1
; GENERAL INFORMATION:
;  APPLICANT: Liou, Simon
;  TITLE OF INVENTION: Human BMP2 Inducible Kinases
;  FILE REFERENCE: 004974.01015
;  CURRENT APPLICATION NUMBER: US/10/509,422
;  CURRENT FILING DATE:  2004-09-24
;  PRIOR APPLICATION NUMBER: PCT/EP03/080825
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/367,512
;  PRIOR FILING DATE: 2002-03-27
;  PRIOR APPLICATION NUMBER: US 60/406,936
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3507
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-509-422-1

  Query Match             24.7%;  Score 23;  DB 1;  Length 3507;
  Best Local Similarity   46.8%;  Pred. No. 53;
  Matches   22;  Conservative   10;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGU 48
              |:| : |  | |  || |:       ||:||:||:||:||:||:||:
Db       1509 CTGCTGCATATAAGCATCTTGAAGTAGGTGGTGGTGGTGGTGGTGGT 1463


RESULT 9
US-10-509-422-3/c
; Sequence 3, Application US/10509422
; Publication No. US20050244825A1
; GENERAL INFORMATION:
;  APPLICANT: Liou, Simon
;  TITLE OF INVENTION: Human BMP2 Inducible Kinases
;  FILE REFERENCE: 004974.01015
;  CURRENT APPLICATION NUMBER: US/10/509,422
;  CURRENT FILING DATE:  2004-09-24
;  PRIOR APPLICATION NUMBER: PCT/EP03/080825
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/367,512
;  PRIOR FILING DATE: 2002-03-27
;  PRIOR APPLICATION NUMBER: US 60/406,936
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3704
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-509-422-3

  Query Match             24.7%;  Score 23;  DB 1;  Length 3704;
  Best Local Similarity   46.8%;  Pred. No. 54;
  Matches   22;  Conservative   10;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGU 48
              |:| : |  | |  || |:       ||:||:||:||:||:||:||:
Db       1609 CTGCTGCATATAAGCATCTTGAAGTAGGTGGTGGTGGTGGTGGTGGT 1563


RESULT 10
US-11-005-030-1/c
; Sequence 1, Application US/11005030
; Publication No. US20050255495A1
; GENERAL INFORMATION:
;  APPLICANT: Aerssens, Jeroen
;  APPLICANT:  Athanasiou, Maria
;  APPLICANT:  Brain, Carlos
;  APPLICANT:  Cohen, Nadine
;  APPLICANT:  Dain, Bradley
;  APPLICANT:  Denton, R. Rex
;  APPLICANT:  Judson, Richard S.
;  APPLICANT:  Ozdemir, Vural
;  APPLICANT:  Reed, Carol R.
```

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;  TITLE OF INVENTION: SLC5A7 Genetic Markers Associated with Age of Onset of
;  TITLE OF INVENTION:  Alzheimer's Disease
;  FILE REFERENCE: 2300.0090001
;  CURRENT APPLICATION NUMBER: US/11/005,030
;  CURRENT FILING DATE:  2004-12-07
;  PRIOR APPLICATION NUMBER: US 60/529,999
;  PRIOR FILING DATE: 2003-12-15
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 26323
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1973)..(1973)
;   OTHER INFORMATION: n is 'g' or 'a'
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2010)..(2010)
;   OTHER INFORMATION: n is 't' or 'c'
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2273)..(2273)
;   OTHER INFORMATION: n is 'a' or 'g'
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2417)..(2417)
;   OTHER INFORMATION: n is 't' or 'c'
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (7671)..(7671)
;   OTHER INFORMATION: n is 'g' or 't'
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16520)..(16520)
;   OTHER INFORMATION: n is 'c' or 't'
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;   NAME/KEY: misc_feature
;   LOCATION: (16546)..(16546)
;   OTHER INFORMATION: n is 'g' or 'a'
US-11-005-030-1

  Query Match             24.7%;  Score 23;  DB 7;  Length 26323;
  Best Local Similarity   47.9%;  Pred. No. 83;
  Matches   34;  Conservative    7;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          19 CUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGUAAA 78
               |:|    |   | :|| ||  |:|| ||  | : || |||| |   : |  ||  | |: ||
Db       23951 CTGGGACCTGTTGGGGGGCGTGGGGGGTGGTGCAAGGAAGGAACTTAGAGGACGGGTCAA 23892

Qy          79 AAACUGCAGGA 89
                 |  :|||| |
Db       23891 TAGGTGCAGCA 23881


RESULT 11
US-10-667-295-44/c
; Sequence 44, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
;  APPLICANT: Mascia, Peter
;  TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
;  FILE REFERENCE: 11696-047001
;  CURRENT APPLICATION NUMBER: US/10/667,295
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: US 60/411,823
;  PRIOR FILING DATE: 2002-09-17
;  NUMBER OF SEQ ID NOS: 263
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
;   LENGTH: 481
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(481)
;   OTHER INFORMATION: Ceres Seq. ID no. 6425497
US-10-667-295-44

  Query Match             24.3%;  Score 22.6;  DB 1;  Length 481;
  Best Local Similarity   41.5%;  Pred. No. 46;
  Matches   22;  Conservative   12;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          25 CACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGUAA 77
               ||| | | :           |: |: |:: ||:||||  : :: | :|||:|| :||
Db         399 CACTGGGTTCTCTTGAGTTGTTGTTTCATGGAAAATCTTAAGTGGCTGCCTAA 347


RESULT 12
US-10-821-234-119/c
; Sequence 119, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 119
;   LENGTH: 2218
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-119

  Query Match             24.3%;  Score 22.6;  DB 1;  Length 2218;
  Best Local Similarity   51.4%;  Pred. No. 65;
  Matches   19;  Conservative    9;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          28 GGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUG 64
               ||:||:||:||:||:||: |   || ||    :|::|
Db        1753 GGTGGTGGTGGTGGTGGTTGAGACAGGGTCTCTGTTG 1717


RESULT 13
US-10-509-921-9/c
; Sequence 9, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
;  APPLICANT: SmithKline Beecham Corporation
;  TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
;  FILE REFERENCE: P51335
;  CURRENT APPLICATION NUMBER: US/10/509,921
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: 60/369,685
;  PRIOR FILING DATE: 2002-04-03
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 7979
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
;   OTHER INFORMATION: HCV J4(B/RI) Replicons
US-10-509-921-9

  Query Match             24.3%;  Score 22.6;  DB 1;  Length 7979;
  Best Local Similarity   43.5%;  Pred. No. 86;
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  Matches   30;  Conservative   10;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:      || |   |:  : | | |:|| ||:||:  :|| ||  || :|| | |:|
Db       5734 CTGTCAGGACAACCGTCCTCTTTCTCCGTGGAGGTGGTATTGGAGGAGCCTTGGTAGGTG 5675

Qy         62 UUGAAUGGC 70
                |  |||
Db       5674 GCAATGGGC 5666


RESULT 14
US-10-509-921-10/c
; Sequence 10, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
;  APPLICANT: SmithKline Beecham Corporation
;  TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
;  FILE REFERENCE: P51335
;  CURRENT APPLICATION NUMBER: US/10/509,921
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: 60/369,685
;  PRIOR FILING DATE: 2002-04-03
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 7979
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
;   OTHER INFORMATION: HCV J4(J4B/R1(C))Replicons
US-10-509-921-10

  Query Match             24.3%;  Score 22.6;  DB 1;  Length 7979;
  Best Local Similarity   43.5%;  Pred. No. 86;
  Matches   30;  Conservative   10;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:      || |   |:  : | | |:|| ||:||:  :|| ||  || :|| | |:|
Db       5734 CTGTCAGGACAACCGTCCTCTTTCTCCGTGGAGGTGGTATTGGAGGAGCCTTGGTAGGTG 5675

Qy         62 UUGAAUGGC 70
                |  |||
Db       5674 GCAATGGGC 5666


RESULT 15
US-10-509-921-11/c
; Sequence 11, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
;  APPLICANT: SmithKline Beecham Corporation
;  TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
;  FILE REFERENCE: P51335
;  CURRENT APPLICATION NUMBER: US/10/509,921
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: 60/369,685
;  PRIOR FILING DATE: 2002-04-03
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 7979
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
;   OTHER INFORMATION: HCV J4 Replicons
US-10-509-921-11

  Query Match             24.3%;  Score 22.6;  DB 1;  Length 7979;
  Best Local Similarity   43.5%;  Pred. No. 86;
  Matches   30;  Conservative   10;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
              |:|:      || |   |:  : | | |:|| ||:||:  :|| ||  || :|| | |:|
Db       5734 CTGTCAGGACAACCGTCCTCTTTCTCCGTGGAGGTGGTATTGGAGGAGCCTTGGTAGGTG 5675

Qy         62 UUGAAUGGC 70
                |  |||
Db       5674 GCAATGGGC 5666


Search completed: November 24, 2005, 04:56:48
Job time : 196 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:35:17 ; Search time 1177.67 Seconds
(without alignments)
4488.911 Million cell updates/sec

Title: US-09-475-158A-16
Perfect score: 93
Sequence: 1 gcuguuuccgaaaucggugg.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	93	100.0	93	6	BD266834	BD266834 PTH funct
	2	73.8	79.4	93	6	BD266832	BD266832 PTH funct
	3	64.2	69.0	93	6	BD266833	BD266833 PTH funct
	4	53.6	57.6	258	6	AR269042	AR269042 Sequence
c	5	48.4	52.0	74	6	AR043802	AR043802 Sequence
	6	46.2	49.7	141	6	AR005132	AR005132 Sequence
c	7	46.2	49.7	141	6	AR005133	AR005133 Sequence
	8	46.2	49.7	141	6	AR177779	AR177779 Sequence
c	9	46.2	49.7	141	6	AR177780	AR177780 Sequence
	10	46.2	49.7	207	6	AR043797	AR043797 Sequence
	11	44.6	48.0	717	6	A36847	A36847 Sequence 1
	12	44.6	48.0	945	6	A36849	A36849 Sequence 3
	13	44	47.3	405	6	BD234383	BD234383 Recombina
	14	44	47.3	408	6	BD234385	BD234385 Recombina
	15	44	47.3	408	6	BD234386	BD234386 Recombina
	16	44	47.3	411	6	BD234384	BD234384 Recombina
	17	44	47.3	414	6	BD234390	BD234390 Recombina
	18	44	47.3	417	6	BD234387	BD234387 Recombina
	19	44	47.3	423	6	BD234388	BD234388 Recombina
	20	44	47.3	435	6	BD234389	BD234389 Recombina
	21	43.4	46.7	45	6	BD073301	BD073301 Recombina
	22	43.4	46.7	45	6	AR269023	AR269023 Sequence
	23	43	46.2	67	6	A79761	A79761 Sequence 9
	24	43	46.2	67	6	AR135774	AR135774 Sequence
c	25	41.4	44.5	71	6	BD234410	BD234410 Recombina
	26	39.8	42.8	234	6	AR027007	AR027007 Sequence
	27	39.8	42.8	234	6	AR027049	AR027049 Sequence
	28	39.8	42.8	234	6	E05661	E05661 DNA encodin
	29	39.8	42.8	234	6	E05676	E05676 DNA encodin
	30	39.8	42.8	237	6	AR027008	AR027008 Sequence
	31	39.8	42.8	237	6	E05662	E05662 DNA encodin
	32	39.8	42.8	240	6	AR027009	AR027009 Sequence
	33	39.8	42.8	240	6	E05663	E05663 DNA encodin
	34	39.8	42.8	243	6	AR027010	AR027010 Sequence
	35	39.8	42.8	243	6	E05664	E05664 DNA encodin
	36	39.8	42.8	245	6	AR027012	AR027012 Sequence
	37	39.8	42.8	245	6	E05659	E05659 DNA encodin
c	38	39.8	42.8	247	6	AR027013	AR027013 Sequence
c	39	39.8	42.8	247	6	E05660	E05660 DNA encodin
	40	39.8	42.8	248	6	AR027014	AR027014 Sequence
	41	39.8	42.8	248	6	E05665	E05665 DNA encodin
c	42	39.8	42.8	250	6	AR027015	AR027015 Sequence
c	43	39.8	42.8	250	6	E05666	E05666 DNA encodin
	44	39.8	42.8	251	6	AR027016	AR027016 Sequence
	45	39.8	42.8	251	6	E05667	E05667 DNA encodin

ALIGNMENTS

RESULT 1
BD266834
LOCUS BD266834 93 bp RNA linear PAT 17-JUL-2003
DEFINITION PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.
ACCESSION BD266834
VERSION BD266834.1 GI:33076602
KEYWORDS JP 2002533115-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 93)
AUTHORS Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
TITLE PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules
JOURNAL Patent: JP 2002533115-A 3 08-OCT-2002;
THE GENERAL HOSPITAL CORP
COMMENT OS Artificial Sequence
PN JP 2002533115-A/3
PD 08-OCT-2002
PF 30-DEC-1999 JP 2000591171
PR 31-DEC-1998 US 60/114577
PI THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD PI JUEPPNER
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC A61P19/10,
PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
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FT source 1. .93
FT /organism='Artificial Sequence'.
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source 1. .93
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/db_xref="taxon:32630"
ORIGIN

Query Match 100.0%; Score 93; DB 6; Length 93;

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  Matches   67;  Conservative   26;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||:|:::|||||:|||:||:||:||:||:||:||:||:|:||||:|||:||||||:
Db          1 GCTGTTTCCGAAATCGGTGGTGGTGGTGGTGGTGGTGGTCTGAACTCCATGGAACGT 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |::|||:|||:|||:|||||||:||||||::
Db         61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 2
BD266832
LOCUS       BD266832                  93 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules.
ACCESSION   BD266832
VERSION     BD266832.1  GI:33076600
KEYWORDS    JP 2002533115-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
  TITLE     PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules
  JOURNAL   Patent: JP 2002533115-A 1 08-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002533115-A/1
            PD   08-OCT-2002
            PF   30-DEC-1999 JP 2000591171
            PR   31-DEC-1998 US    60/114577
            PI   THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD  PI
            JUEPPNER
            PC   C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC
              A61P19/10,
            PC   A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
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ORIGIN

  Query Match             79.4%;  Score 73.8;  DB 6;  Length 93;
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  Matches   59;  Conservative   22;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||:|:::|||||:|           ||:||:||:||:||:|:||||:|||:||||||:
Db          1 GCTGTTTCCGAAATCCAGCTGATGCACGGTGGTGGTGGTGGTCTGAACTCCATGGAACGT 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |::|||:|||:|||:|||||||:||||||::
Db         61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 3
BD266833
LOCUS       BD266833                  93 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules.
ACCESSION   BD266833
VERSION     BD266833.1  GI:33076601
KEYWORDS    JP 2002533115-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 93)
  AUTHORS   Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
  TITLE     PTH functional domain conjugate peptides, derivatives thereof and
            novel tethered ligand-receptor molecules
  JOURNAL   Patent: JP 2002533115-A 2 08-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002533115-A/2
            PD   08-OCT-2002
            PF   30-DEC-1999 JP 2000591171
            PR   31-DEC-1998 US    60/114577
            PI   THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD  PI
            JUEPPNER
            PC   C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC
              A61P19/10,
            PC   A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
            Description of Artificial Sequence: modified PTH sequence FH   Key
                     Location/Qualifiers
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ORIGIN

  Query Match             69.0%;  Score 64.2;  DB 6;  Length 93;
  Best Local Similarity   58.1%;  Pred. No. 3.7e-08;
  Matches   54;  Conservative   21;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||:|:::|||||:|           ||:||:||:||:||:      :|||:||||||:
Db          1 GCTGTTTCCGAAATCCAGCTGATGCACGGTGGTGGTGGTGGTGGTGGTTCCATGGAACGT 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |::|||:|||:|||:|||||||:||||||::
Db         61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 4
AR269042
LOCUS       AR269042                  258 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 26 from patent US 6500647.
ACCESSION   AR269042
VERSION     AR269042.1  GI:29699873
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 258)
  AUTHORS   Jung,E.-K., Park,D.-H. and Chung,S.-I.
  TITLE     Recombinant expression vector of human parathyroid hormone
  JOURNAL   Patent: US 6500647-A 26 31-DEC-2002;
            Mogam Biotechnology Research Institute; Kyonggi-Do;
            KRX;
FEATURES             Location/Qualifiers
     source          1. .258
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             57.6%;  Score 53.6;  DB 6;  Length 258;
  Best Local Similarity   51.1%;  Pred. No. 4.6e-05;
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Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|     :      :      ||:     :|:||||:| |:||||||:|
```

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Db          2 CTGTTTCGGAAATCCAGCTTATGCATAACCTGGGTAAACATCTGAACTCGATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:|||||| |::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGATGTT 93


RESULT 5
AR043802/c
LOCUS       AR043802                  74 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 132 from patent US 5814603.
ACCESSION   AR043802
VERSION     AR043802.1  GI:5964810
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Oldenburg,K.R. and Selick,H.E.
  TITLE     Compounds with PTH activity
  JOURNAL   Patent: US 5814603-A 132 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .74
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             52.0%;  Score 48.4;  DB 6;  Length 74;
  Best Local Similarity   74.0%;  Pred. No. 0.0015;
  Matches   37;  Conservative   12;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         44 UGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              :||||:|| :||||||:|::|||:|||:|||:|||||||:||||||::
Db         74 TGAACTCCCTGGAACGTGTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 25


RESULT 6
AR005132
LOCUS       AR005132                 141 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5747453.
ACCESSION   AR005132
VERSION     AR005132.1  GI:3966011
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 5747453-A 3 05-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             49.7%;  Score 46.2;  DB 6;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 0.0064;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                    ||:      |:||||:|| : || ||:|
Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||:
Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 7
AR005133/c
LOCUS       AR005133                 141 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5747453.
ACCESSION   AR005133
VERSION     AR005133.1  GI:3966012
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 5747453-A 5 05-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             49.7%;  Score 46.2;  DB 6;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 0.0064;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                    ||:      |:||||:|| : || ||:|
Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 8
AR177779
LOCUS       AR177779                 141 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 3 from patent US 6313092.
ACCESSION   AR177779
VERSION     AR177779.1  GI:17920134
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 6313092-A 3 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             49.7%;  Score 46.2;  DB 6;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 0.0064;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                    ||:      |:||||:|| : || ||:|
Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||:
Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 9
AR177780/c
LOCUS       AR177780                 141 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 5 from patent US 6313092.
ACCESSION   AR177780
VERSION     AR177780.1  GI:17920135
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
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  AUTHORS   Holladay,L.A. and Oldenburg,K.R.
  TITLE     Method for increasing the electrotransport flux of polypeptides
  JOURNAL   Patent: US 6313092-A 5 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             49.7%;  Score 46.2;  DB 6;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 0.0064;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                ||:      |:||||:|| : || ||:|
Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 10
AR043797
LOCUS       AR043797                207 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5814603.
ACCESSION   AR043797
VERSION     AR043797.1  GI:5964805
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 207)
  AUTHORS   Oldenburg,K.R. and Selick,H.E.
  TITLE     Compounds with PTH activity
  JOURNAL   Patent: US 5814603-A 8 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .207
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             49.7%;  Score 46.2;  DB 6;  Length 207;
  Best Local Similarity   51.6%;  Pred. No. 0.0065;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                ||:      |:||||:|| : || ||:|
Db         71 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 130

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db        131 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 161


RESULT 11
A36847
LOCUS       A36847                  717 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 1 from Patent WO9402510.
ACCESSION   A36847
VERSION     A36847.1  GI:2294105
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Bauer,W., Breckenridge,R., Cardinaux,F., Gombert,F., Gram,H.,
            Ramage,P., Schneider,H., Waelchli,R., Albert, Rainer and Lewis,I.
  TITLE     ANALOGS OF PTH
  JOURNAL   Patent: WO 9402510-A 1 03-FEB-1994;
            SANDOZ AG (AT)
COMMENT     Other publication HU 70459 951030
            Other publication CZ 9500088 951018
            Other publication AU 4156693 940120
            Other publication SK 4395 950607
            Other publication NZ 248137 951221
            Other publication GB 2269176 940202
            Other publication JP 6184198 940705
            Other publication CA 2100423 940116
            Other publication CN 1099801 950308
            Other publication DE 4393381T 950427
            Other publication NO 950123 950315
            Other publication ZA 9305126 950116
            Other publication FI 950171 950313.
FEATURES             Location/Qualifiers
     source          1. .717
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
     CDS             101. .562
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAA02267.1"
                     /db_xref="GI:2294106"
                     /translation="MSETKPKYNYVNNKELLQAIIDWKTELANNKDPNKVVRQNDTIG
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ORIGIN

  Query Match             48.0%;  Score 44.6;  DB 6;  Length 717;
  Best Local Similarity   49.5%;  Pred. No. 0.019;
  Matches   45;  Conservative   17;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |: :| ||||:                :  :   ||:     :|:||| :| |:|||||:|
Db        447 CCGTATCAGAAATACAACTAATGCATAATCTGGGTAAACATCTGAATTCAATGGAACGTG 506

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|||||||:|||||| |:
Db        507 TAGAATGGCTGCGTAAAAAACTGCAGGATGT 537


RESULT 12
A36849
LOCUS       A36849                  945 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 3 from Patent WO9402510.
ACCESSION   A36849
VERSION     A36849.1  GI:2294107
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   Bauer,W., Breckenridge,R., Cardinaux,F., Gombert,F., Gram,H.,
            Ramage,P., Schneider,H., Waelchli,R., Albert, Rainer and Lewis,I.
  TITLE     ANALOGS OF PTH
  JOURNAL   Patent: WO 9402510-A 3 03-FEB-1994;
            SANDOZ AG (AT)
COMMENT     Other publication HU 70459 951030
            Other publication CZ 9500088 951018
            Other publication AU 4156693 940120
            Other publication SK 4395 950607
            Other publication NZ 248137 951221
            Other publication GB 2269176 940202
            Other publication JP 6184198 940705
            Other publication CA 2100423 940116
            Other publication CN 1099801 950308
            Other publication DE 4393381T 950427
            Other publication NO 950123 950315
            Other publication ZA 9305126 950116
            Other publication FI 950171 950313.
FEATURES             Location/Qualifiers
     source          1. .945
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
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                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAA02268.1"
                     /db_xref="GI:2294108"
                     /translation="MSETKPKYNYVNNKELLQAIIDWKTELANNKDPNKVVRQNDTIG
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                     FNAFVQRIKKERKEVAKKYSYFVHNVYDSRDDDMVALVDETFIQDIYDKMTHYEESTY
                     RTPGAEKKSVVDDSPSLDFLYEANDGSVNGPSVSEIQLMHNLGKHLNSMERVEWLRKK
                     LQDVHNFVALG"
ORIGIN

  Query Match             48.0%;  Score 44.6;  DB 6;  Length 945;
  Best Local Similarity   49.5%;  Pred. No. 0.019;
  Matches   45;  Conservative   17;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |: :| ||||:            :  :   ||:     :|:||| :| |:||||||:|
Db        675 CCGTATCAGAAATACAACTAATGCATAATCTGGGTAAACATCTGAATTCAATGGAACGTG 734

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : |||:|||:|||:|||||||:|||||| |:
Db        735 TAGAATGGCTGCGTAAAAAACTGCAGGATGT 765


RESULT 13
BD234383
LOCUS       BD234383                405 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234383
VERSION     BD234383.1  GI:33044153
KEYWORDS    JP 2002533072-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 4 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/4
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: PCpB-RVR-hPTH fusion FH
            Key             Location/Qualifiers
            FT   CDS             (4). .(393).
FEATURES            Location/Qualifiers
     source         1. .405
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
ORIGIN

  Query Match             47.3%;  Score 44;  DB 6;  Length 405;
  Best Local Similarity   47.8%;  Pred. No. 0.029;
  Matches   44;  Conservative   18;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
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Db        293 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 352

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              : |||:|||:|||:|| || |:|||||| |::
Db        353 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 384


RESULT 14
BD234385
LOCUS       BD234385                408 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234385
VERSION     BD234385.1  GI:33044155
KEYWORDS    JP 2002533072-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 6 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/6
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: PCpB-IEGR-hPTH fusion FH
            Key             Location/Qualifiers
            FT   CDS             (4). .(396).
FEATURES            Location/Qualifiers
     source         1. .408
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
ORIGIN

  Query Match             47.3%;  Score 44;  DB 6;  Length 408;
  Best Local Similarity   47.8%;  Pred. No. 0.029;
  Matches   44;  Conservative   18;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|           :      ||      :|:||||:| |:||| ||:|
Db        296 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 355

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              : |||:|||:|||:|| || |:|||||| |::
Db        356 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 387


RESULT 15
BD234386
LOCUS       BD234386                408 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant synthesis of beta-lipotropin and other peptides.
ACCESSION   BD234386
VERSION     BD234386.1  GI:33044156
KEYWORDS    JP 2002533072-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Hale,J.E., Hershberger,C.L., Larson,J.L. and Menke,M.A.
  TITLE     Recombinant synthesis of beta-lipotropin and other peptides
  JOURNAL   Patent: JP 2002533072-A 7 08-OCT-2002;
            ELI LILLY AND CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002533072-A/7
            PD   08-OCT-2002
            PF   15-DEC-1999 JP 2000589671
            PR   21-DEC-1998 US    60/113058
            PI   JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
            PI   MICHAEL ANDREW MENKE
            PC   C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/50,
            PC   C12P21/02,C12N15/00,C12N5/00
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           CC   Description of Artificial Sequence: PCpB-LVPR-hPTH fusion FH
           Key              Location/Qualifiers
           FT   CDS              (4). .(396).
FEATURES             Location/Qualifiers
     source          1. .408
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             47.3%;  Score 44;  DB 6;  Length 408;
  Best Local Similarity   47.8%;  Pred. No. 0.029;
  Matches   44;  Conservative   18;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|           :       ||       :|:||||:| |:||| ||:|
Db        296 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 355

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
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Db        356 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 387


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GenCore version 5.1.6

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Listing first 45 summaries

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SUMMARIES

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2	73.8	79.4	93	3	AAA51729	Aaa51729 PTH funct
3	64.2	69.0	93	3	AAA51730	Aaa51730 PTH funct
4	52	55.9	152	2	AAT73910	Aat73910 Synthetic
5	52	55.9	489	12	ADG48030	Adg48030 Human PTH
6	52	55.9	489	12	ADG48059	Adg48059 Human PTH
7	52	55.9	489	12	ADG68786	Adg68786 Human mut
8	50.4	54.2	102	12	ADG93179	Adg93179 Novel exp
9	50.4	54.2	102	12	ADJ65857	Adj65857 PTH pepti
10	50.4	54.2	102	13	ADW14377	Adw14377 Human par
11	50.4	54.2	111	12	ADG93180	Adg93180 Novel exp
12	50.4	54.2	111	12	ADJ65858	Adj65858 PTH pepti
13	50.4	54.2	111	13	ADW14375	Adw14375 Human par
14	50.4	54.2	117	12	ADG93260	Adg93260 Novel exp
15	50.4	54.2	168	2	AAT34865	Aat34865 Plasmid p
16	50.4	54.2	252	12	ADG93181	Adg93181 Novel exp
17	50.4	54.2	252	12	ADJ65859	Adj65859 PTH prote
18	50.4	54.2	264	12	ADJ65913	Adj65913 Tandem po
19	50.4	54.2	276	12	ADF90345	Adf90345 Chimeric
20	50.4	54.2	276	12	ADJ65899	Adj65899 PTH DNA s
21	50.4	54.2	276	12	ADJ87051	Adj87051 Nucleotid
22	50.4	54.2	282	12	ADG93252	Adg93252 Novel exp
23	50.4	54.2	291	12	ADJ65901	Adj65901 PTH DNA s
24	50.4	54.2	291	12	ADJ65900	Adj65900 PTH DNA s
25	50.4	54.2	294	2	AAT34866	Aat34866 Plasmid p
26	50.4	54.2	321	12	ADJ65915	Adj65915 Tandem po
27	50.4	54.2	420	12	ADJ65917	Adj65917 Tandem po
28	50.4	54.2	426	12	ADF90347	Adf90347 Chimeric
29	50.4	54.2	528	6	AAS19702	Aas19702 DNA encod
30	49.4	53.1	108	13	ADV69494	Adv69494 Human par
31	49.4	53.1	114	13	ADV69502	Adv69502 Human par
32	46.4	49.9	52	13	ADV69498	Adv69498 Human par
33	46.2	49.7	141	2	AAQ89920	Aaq89920 Recombina
34	46.2	49.7	141	2	AAT80383	Aat80383 rPTH codi
35	46.2	49.7	207	2	AAQ89923	Aaq89923 Expressio
36	45.2	48.6	145	13	ADW80822	Adw80822 DNA encod
c 37	44.6	48.0	76	12	ADO42786	Ado42786 Human PTH
38	44.6	48.0	728	2	AAQ55301	Aaq55301 Truncated
39	44.6	48.0	945	2	AAQ55302	Aaq55302 gp55-Asn-
40	44	47.3	405	3	AAA51452	Aaa51452 PCpB-RVR-
41	44	47.3	408	3	AAA51455	Aaa51455 PCpB-LVPR
42	44	47.3	408	3	AAA51454	Aaa51454 PCpB-IEGR
43	44	47.3	411	3	AAA51453	Aaa51453 PCpB-ALY-
44	44	47.3	414	3	AAA51459	Aaa51459 PCpB-APR-
45	44	47.3	417	3	AAA51456	Aaa51456 PCpB-VIPR

ALIGNMENTS

RESULT 1
AAA51731
ID AAA51731 standard; RNA; 93 BP.
XX
AC AAA51731;
XX
DT 31-OCT-2000 (first entry)
XX
DE PTH functional domain conjugate peptide PG9 coding sequence.
XX
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW resorption; remodeling; tether1; osteoporosis; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .93
FT /*tag= a
FT /product= "PG9"
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
DR P-PSDB; AAY96974.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.

```
XX
PS   Claim 14; Fig 1; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 93 BP; 18 A; 14 C; 35 G; 0 T; 26 U; 0 Other;

  Query Match             100.0%;  Score 93;  DB 3;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-19;
  Matches   93;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |||||||||||||||||||||||||||||||||
Db         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93


RESULT 2
AAA51729
ID   AAA51729 standard; RNA; 93 BP.
XX
AC   AAA51729;
XX
DT   31-OCT-2000  (first entry)
XX
DE   PTH functional domain conjugate peptide PG5 coding sequence.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .93
FT                   /*tag=  a
FT                   /product= "PG5"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   P-PSDB; AAY96973.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 14; Fig 1; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 93 BP; 21 A; 18 C; 30 G; 0 T; 24 U; 0 Other;

  Query Match             79.4%;  Score 73.8;  DB 3;  Length 93;
  Best Local Similarity   87.1%;  Pred. No. 2.5e-13;
  Matches   81;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||||||||||||||||           ||||||||||||||||||||||||||||||||
Db          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60

Qy         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              |||||||||||||||||||||||||||||||||
Db         61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93


RESULT 3
AAA51730
ID   AAA51730 standard; RNA; 93 BP.
XX
AC   AAA51730;
XX
DT   31-OCT-2000  (first entry)
XX
DE   PTH functional domain conjugate peptide PG7 coding sequence.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .93
FT                   /*tag=  a
FT                   /product= "PG7"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   P-PSDB; AAY96975.
```

```
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 14; Fig 1; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 93 BP; 19 A; 16 C; 33 G; 0 T; 25 U; 0 Other;

  Query Match             69.0%;  Score 64.2;  DB 3;  Length 93;
  Best Local Similarity   80.6%;  Pred. No. 2.5e-10;
  Matches   75;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GCUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
              ||||||||||||||||            ||||||||||||||||      ||||||||||||
Db          1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60

Qy         61 GUUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              |||||||||||||||||||||||||||||||||||
Db         61 GUUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93


RESULT 4
AAT73910
ID   AAT73910 standard; DNA; 152 BP.
XX
AC   AAT73910;
XX
DT   25-MAR-2003  (revised)
DT   30-JAN-1998  (first entry)
XX
DE   Synthetic oligonucleotide encoding linker and PTH 1-37.
XX
KW   Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein;
KW   recombinant production; endoproteinase LysC; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .4
FT                   /*tag=  b
FT                   /label= sticky_end
FT                   /note= "5' end of complementary strand overhangs 3' end
FT                   of present strand by sequence 5'-TCGA-3'"
FT   CDS             6. .152
FT                   /*tag=  a
XX
PN   WO9718314-A1.
XX
PD   22-MAY-1997.
XX
PF   06-NOV-1996;   96WO-EP004850.
XX
PR   16-NOV-1995;   95DE-01042702.
XX
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI   Kopetzki E;
XX
DR   WPI; 1997-289290/26.
DR   P-PSDB; AAW21946.
XX
PT   Recombinant production of peptide(s) as fusions with streptavidin
PT   attached via cleavable linker - especially for urotropin and parathyroid
PT   hormone production.
XX
PS   Example 2; Fig 2; 37pp; German.
XX
CC   The present sequence, which encodes a linker and the parathyroid hormone
CC   1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was
CC   ligated to the 2.9 kb NheI-HindIII fragment of pSAM-CORE, which contains
CC   the Met(13-139) streptavidin (SA) sequence, to give pSA-EK-PTH. pSA-EK-
CC   PTH and the LacIq repressor plasmid pUBS500 were used to transform E.
CC   coli K12 RM82. The transformants were grown, with IPTG induction, in
CC   medium containing kanamycin and ampilcilin. Cells were harvested, lysed
CC   and isolated inclusion bodies solubilised in guanidine hydrochloride, and
CC   renatured by dilution in pH 7 phosphate buffer. The solution was
CC   clarified and the supernatant concentrated and purified on a column of
CC   immobilised iminobiotin. The purified material was incubated with
CC   endoproteinase LysC and the PTH 1-37 fragment released, recovered by SA
CC   fragment removal on an iminobiotin column followed by chromatography on a
CC   fractogel and reverse phase HPLC. The endoproteinase LysC cleaves the
CC   fusion protein rapidly and completely, exclusively at the Lys residue in
CC   the linker, i.e. not at Lys residues in SA. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;

  Query Match             55.9%;  Score 52;  DB 2;  Length 152;
  Best Local Similarity   54.3%;  Pred. No. 1.8e-06;
  Matches   50;  Conservative   17;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                  ||:      |:||||:|||:||||||:|
Db         37 CCGTTTCCGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCCATGGAACGTG 96

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         97 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 128


RESULT 5
ADG48030
ID   ADG48030 standard; DNA; 489 BP.
XX
AC   ADG48030;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human PTH-TTR (C10A/K15A/G83C) variant fusion DNA.
XX
KW   Transthyretin; TTR; thrombopoietin mimetic peptide; TPO; TMP;
KW   thrombocytopaenia; megakaryocyte deficiency; platelet deficiency;
KW   thrombocytopaenia; aplastic anaemia; idiopathic thrombocytopaenia;
KW   metastatic tumours; systemic lupus erythematosus; splenomegaly;
KW   Fanconi's syndrome; vitamin B12 deficiency; folic acid deficiency;
KW   May-Hegglin anomaly; Wiskott-Aldrich syndrome;
KW   paroxysmal nocturnal haemoglobinuria; glucagon-like peptide 1; GLP-1;
KW   non-insulin dependent diabetes; haemostatic; dermatological;
KW   immunosuppressive; antiinflammatory; cytostatic; mutant; variant;
KW   parathyroid hormone; PTH; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003195154-A1.
XX
PD   16-OCT-2003.
XX
PF   03-APR-2003; 2003US-00407078.
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```
XX
PR   04-APR-2002; 2002US-00117109.
XX
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
XX
PI   Walker K,  Xiong F;
XX
DR   WPI; 2004-051257/05.
XX
PT   Increasing serum half-life of biologically active agent involves fusing
PT   biologically active agent to transthyretin or a transthyretin variant.
XX
PS   Example 3; SEQ ID NO 14; 61pp; English.
XX
CC   The present invention relates to a method of increasing the serum half-
CC   life of a biologically active agent involves fusing the biologically
CC   active agent to transthyretin (TTR) or a TTR variant. The method is
CC   useful for increasing the serum half-life of a biologically active agent.
CC   Homogenous compositions comprising thrombopoietin (TPO) mimetic peptide
CC   (TMP) is useful for treating thrombocytopaenia, megakaryocyte/platelet
CC   deficiency/thrombocytopaenia, diseases that involve thrombocytopenia
CC   e.g., aplastic anaemia, idiopathic thrombocytopaenia, metastatic tumours
CC   which result in thrombocytopaenia, systemic lupus erythematosus,
CC   splenomegaly, Fanconi's syndrome, vitamin B12 deficiency, folic acid
CC   deficiency, May-Hegglin anomaly, Wiskott-Aldrich syndrome and paroxysmal
CC   nocturnal haemoglobinuria. Homogenous compositions comprising glucagon-
CC   like peptide 1 (GLP-1) is useful for treating non-insulin dependent
CC   diabetes. TMP compounds are useful in stimulating certain cell types
CC   other than megakaryocyte, which expresses Mpl receptor and in maintaining
CC   the viability or storage life of platelets and related cells. The present
CC   sequence is human parathyroid hormone (PTH)-TTR variant fusion DNA.
XX
SQ   Sequence 489 BP; 123 A; 128 C; 123 G; 115 T; 0 U; 0 Other;

  Query Match             55.9%;  Score 52;  DB 12;  Length 489;
  Best Local Similarity   51.1%;  Pred. No. 2.3e-06;
  Matches   47;  Conservative   20;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|          :       ||:     :|:||||:| |:||||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGTAAACATCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|| ||||:||||||||::
Db         65 TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96


RESULT 6
ADG48059
ID   ADG48059 standard; DNA; 489 BP.
XX
AC   ADG48059;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human PTH-TTR (C10A/K15A/A81C) variant fusion DNA.
XX
KW   Transthyretin; TTR; thrombopoietin mimetic peptide; TPO; TMP;
KW   thrombocytopaenia; megakaryocyte deficiency; platelet deficiency;
KW   thrombocytopaenia; aplastic anaemia; idiopathic thrombocytopaenia;
KW   metastatic tumours; systemic lupus erythematosus; splenomegaly;
KW   Fanconi's syndrome; vitamin B12 deficiency; folic acid deficiency;
KW   May-Hegglin anomaly; Wiskott-Aldrich syndrome;
KW   paroxysmal nocturnal haemoglobinuria; glucagon-like peptide 1; GLP-1;
KW   non-insulin dependent diabetes; haemostatic; dermatological;
KW   immunosuppressive; antiinflammatory; cytostatic; mutant; variant;
KW   parathyroid hormone; PTH; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003195154-A1.
XX
PD   16-OCT-2003.
XX
PF   03-APR-2003; 2003US-00407078.
XX
PR   04-APR-2002; 2002US-00117109.
XX
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
XX
PI   Walker K,  Xiong F;
XX
DR   WPI; 2004-051257/05.
XX
PT   Increasing serum half-life of biologically active agent involves fusing
PT   biologically active agent to transthyretin or a transthyretin variant.
XX
PS   Example 17; SEQ ID NO 43; 61pp; English.
XX
CC   The present invention relates to a method of increasing the serum half-
CC   life of a biologically active agent involves fusing the biologically
CC   active agent to transthyretin (TTR) or a TTR variant. The method is
CC   useful for increasing the serum half-life of a biologically active agent.
CC   Homogenous compositions comprising thrombopoietin (TPO) mimetic peptide
CC   (TMP) is useful for treating thrombocytopaenia, megakaryocyte/platelet
CC   deficiency/thrombocytopaenia, diseases that involve thrombocytopenia
CC   e.g., aplastic anaemia, idiopathic thrombocytopaenia, metastatic tumours
CC   which result in thrombocytopaenia, systemic lupus erythematosus,
CC   splenomegaly, Fanconi's syndrome, vitamin B12 deficiency, folic acid
CC   deficiency, May-Hegglin anomaly, Wiskott-Aldrich syndrome and paroxysmal
CC   nocturnal haemoglobinuria. Homogenous compositions comprising glucagon-
CC   like peptide 1 (GLP-1) is useful for treating non-insulin dependent
CC   diabetes. TMP compounds are useful in stimulating certain cell types
CC   other than megakaryocyte, which expresses Mpl receptor and in maintaining
CC   the viability or storage life of platelets and related cells. The present
CC   sequence is human parathyroid hormone (PTH)-TTR variant fusion DNA.
XX
SQ   Sequence 489 BP; 123 A; 128 C; 123 G; 115 T; 0 U; 0 Other;

  Query Match             55.9%;  Score 52;  DB 12;  Length 489;
  Best Local Similarity   51.1%;  Pred. No. 2.3e-06;
  Matches   47;  Conservative   20;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|          :       ||:     :|:||||:| |:||||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGTAAACATCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|| ||||:||||||||::
Db         65 TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96


RESULT 7
ADG68786
ID   ADG68786 standard; cDNA; 489 BP.
XX
AC   ADG68786;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human mutant transthyretin (TTR)  cDNA #12.
XX
KW   Human; transthyretin; TTR; gene; ss; TPO mimetic peptide; TMP;
KW   thrombocytopenia; aplastic anaemia; metastatic tumour; cancer;
KW   haemostatic; antianaemic; cytostatic; mutant.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003191056-A1.
XX
PD   09-OCT-2003.
XX
```

```
PF   04-APR-2002; 2002US-00117109.
XX
PR   04-APR-2002; 2002US-00117109.
XX
PA   (WALK/) WALKER K.
PA   (XION/) XIONG F.
XX
PI   Walker K,  Xiong F;
XX
DR   WPI; 2004-010111/01.
XX
PT   Increasing the serum half-life of a biologically active agent for
PT   treating thrombocytopenia, comprises fusing the agent to transthyretin or
PT   a variant of it.
XX
PS   Example 3; SEQ ID NO 14; 35pp; English.
XX
CC   The invention relates to a method for increasing the serum half-life of a
CC   biologically active agent comprising fusing the agent to transthyretin
CC   (TTR) or a TTR variant. The invention also relates to a homogenous
CC   preparation of a TTR-biologically active agent fusion, a polyethylene
CC   glycol (PEG)-TTR-biologically active agent fusion, a TTR variant-
CC   biologically active agent fusion and a PEG-TTR variant-biologically
CC   active agent fusion, optionally in a pharmaceutically acceptable diluent,
CC   carrier or adjuvant. The method is used to increase the serum half-life
CC   of a biologically active agent, e.g. a protein or a peptide. A
CC   preparation comprising a TPO mimetic peptide (TMP) is used to treat
CC   thrombocytopenia, aplastic anaemia and metastatic tumours. This sequence
CC   represents cDNA encoding a human mutant TTR polypeptide of the invention.
XX
SQ   Sequence 489 BP; 123 A; 128 C; 123 G; 115 T; 0 U; 0 Other;

  Query Match             55.9%;  Score 52;  DB 12;  Length 489;
  Best Local Similarity   51.1%;  Pred. No. 2.3e-06;
  Matches   47;  Conservative   20;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|         :      ||:     :|:||||:| |:|||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGTAAACATCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|| ||||:||||||::
Db         65 TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96


RESULT 8
ADG93179
ID   ADG93179 standard; DNA; 102 BP.
XX
AC   ADG93179;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel expression cassette-related polypeptide-encoding DNA SeqID60.
XX
KW   expression cassette; high yield polypeptide production;
KW   tandem polypeptide; inclusion body; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100021-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016643.
XX
PR   24-MAY-2002; 2002US-0383370P.
XX
PA   (REST-) RESTORAGEN INC.
PA   (HARL/) HARLEY S.
XX
PI   Harley S,  Williams JA,  Luan P,  Xia Y;
XX
DR   WPI; 2004-035128/03.
DR   P-PSDB; ADG93159.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 60; 157pp; English.
XX
CC   This invention relates to a novel expression cassette and methods for
CC   high yield production of polypeptides. The cassette comprises an operably
CC   linked nucleic acid sequence, where the expression of the cassette
CC   produces a tandem polypeptide that forms an inclusion body when expressed
CC   in a cell. The expression cassette is useful for producing peptide and
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present sequence is that of
CC   a DNA sequence which encodes a polypeptide which may be produced using
CC   the expression cassette of the invention.
XX
SQ   Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

  Query Match             54.2%;  Score 50.4;  DB 12;  Length 102;
  Best Local Similarity   52.2%;  Pred. No. 5.1e-06;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 9
ADJ65857
ID   ADJ65857 standard; DNA; 102 BP.
XX
AC   ADJ65857;
XX
DT   06-MAY-2004  (first entry)
XX
DE   PTH peptide coding sequence #1.
XX
KW   expression cassette; tandem polypeptide; inclusion body;
KW   inclusion body fusion partner; PTH; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100022-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016645.
XX
PR   24-MAY-2002; 2002US-0383212P.
XX
PA   (REST-) RESTORAGEN INC.
XX
PI   Xia Y,  Peng L;
XX
DR   WPI; 2004-035129/03.
DR   P-PSDB; ADJ65837.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 33; 132pp; English.
XX
CC   The invention comprises an expression cassette which produces a tandem
CC   polypeptide that form an inclusion body when expressed in a cell. The
CC   expression cassette of the invention is useful for producing a peptide or
```

```
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present DNA sequence encodes
CC   a peptide which may be used in the construction of a tandem polypeptide
CC   of the invention.
XX
SQ   Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

  Query Match            54.2%;  Score 50.4;  DB 12;  Length 102;
  Best Local Similarity  52.2%;  Pred. No. 5.1e-06;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 10
ADW14377
ID   ADW14377 standard; DNA; 102 BP.
XX
AC   ADW14377;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human parathyroxin PTH 1-34 peptide encoding DNA SEQ ID NO:3.
XX
KW   ds; parathyroxin; recombinant protein; protein engineering.
XX
OS   Homo sapiens.
XX
PN   CN1424325-A.
XX
PD   18-JUN-2003.
XX
PF   12-DEC-2001; 2001CN-00142627.
XX
PR   12-DEC-2001; 2001CN-00142627.
XX
PA   (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.
XX
PI   Chen C,  Xiu C,  Li M;
XX
DR   WPI; 2004-099606/11.
DR   P-PSDB; ADW14378.
XX
PT   Production of reorganized human parathyroid hormone 1-34 peptide.
XX
PS   Disclosure; SEQ ID NO 3; 25pp; Chinese.
XX
CC   The invention relates to a novel process for preparing recombinant human
CC   parathyroxin 1-34 peptide, including such steps as culturing a host cell
CC   in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376),
CC   severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and
CC   separating and purifying PTH 1-34 peptide. The present sequence encodes
CC   the PTH 1-34 peptide.
XX
SQ   Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;

  Query Match            54.2%;  Score 50.4;  DB 13;  Length 102;
  Best Local Similarity  52.2%;  Pred. No. 5.1e-06;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 11
ADG93180
ID   ADG93180 standard; DNA; 111 BP.
XX
AC   ADG93180;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel expression cassette-related polypeptide-encoding DNA SeqID61.
XX
KW   expression cassette; high yield polypeptide production;
KW   tandem polypeptide; inclusion body; gene; ds.
XX
OS   Unidentified.
XX
PN   WO2003100021-A2.
XX
PD   04-DEC-2003.
XX
PF   23-MAY-2003; 2003WO-US016643.
XX
PR   24-MAY-2002; 2002US-0383370P.
XX
PA   (REST-) RESTORAGEN INC.
PA   (HARL/) HARLEY S.
XX
PI   Harley S,  Williams JA,  Luan P,  Xia Y;
XX
DR   WPI; 2004-035128/03.
DR   P-PSDB; ADG93160.
XX
PT   New expression cassette comprising an operably linked nucleic acid
PT   sequence, useful for producing a tandem polypeptide that forms an
PT   inclusion body when expressed in a cell.
XX
PS   Disclosure; SEQ ID NO 61; 157pp; English.
XX
CC   This invention relates to a novel expression cassette and methods for
CC   high yield production of polypeptides. The cassette comprises an operably
CC   linked nucleic acid sequence, where the expression of the cassette
CC   produces a tandem polypeptide that forms an inclusion body when expressed
CC   in a cell. The expression cassette is useful for producing peptide and
CC   polypeptide in a cell, preferably a tandem polypeptide that forms an
CC   inclusion body when expressed in a cell. The present sequence is that of
CC   a DNA sequence which encodes a polypeptide which may be produced using
CC   the expression cassette of the invention.
XX
SQ   Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;

  Query Match            54.2%;  Score 50.4;  DB 12;  Length 111;
  Best Local Similarity  52.2%;  Pred. No. 5.2e-06;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 12
ADJ65858
ID   ADJ65858 standard; DNA; 111 BP.
XX
AC   ADJ65858;
XX
DT   06-MAY-2004  (first entry)
XX
DE   PTH peptide coding sequence #2.
```

XX
KW expression cassette; tandem polypeptide; inclusion body;
KW inclusion body fusion partner; PTH; gene; ds.
XX
OS Unidentified.
XX
PN WO2003100022-A2.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-US016645.
XX
PR 24-MAY-2002; 2002US-0383212P.
XX
PA (REST-) RESTORAGEN INC.
XX
PI Xia Y, Peng L;
XX
DR WPI; 2004-035129/03.
DR P-PSDB; ADJ65838.
XX
PT New expression cassette comprising an operably linked nucleic acid
PT sequence, useful for producing a tandem polypeptide that forms an
PT inclusion body when expressed in a cell.
XX
PS Disclosure; SEQ ID NO 34; 132pp; English.
XX
CC The invention comprises an expression cassette which produces a tandem
CC polypeptide that form an inclusion body when expressed in a cell. The
CC expression cassette of the invention is useful for producing a peptide or
CC polypeptide in a cell, preferably a tandem polypeptide that forms an
CC inclusion body when expressed in a cell. The present DNA sequence encodes
CC a peptide which may be used in the construction of a tandem polypeptide
CC of the invention.
XX
SQ Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;

Query Match 54.2%; Score 50.4; DB 12; Length 111;
Best Local Similarity 52.2%; Pred. No. 5.2e-06;
Matches 48; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
|:|:::| ||||:| ||: |:||||:| |:||||||:|
Db 2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||:||||||::
Db 62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93

RESULT 13
ADW14375
ID ADW14375 standard; DNA; 111 BP.
XX
AC ADW14375;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human parathyroxin Gly-Ser-Pro-PTH 1-34 peptide DNA SEQ ID NO:1.
XX
KW ds; parathyroxin; recombinant protein; protein engineering.
XX
OS Homo sapiens.
XX
PN CN1424325-A.
XX
PD 18-JUN-2003.
XX
PF 12-DEC-2001; 2001CN-00142627.
XX
PR 12-DEC-2001; 2001CN-00142627.
XX
PA (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.
XX
PI Chen C, Xiu C, Li M;
XX
DR WPI; 2004-099606/11.
DR P-PSDB; ADW14376.
XX
PT Production of reorganized human parathyroid hormone 1-34 peptide.
XX
PS Claim 3; SEQ ID NO 1; 25pp; Chinese.
XX
CC The invention relates to a novel process for preparing recombinant human
CC parathyroxin 1-34 peptide, including such steps as culturing a host cell
CC in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376),
CC severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and
CC separating and purifying PTH 1-34 peptide. The present sequence encodes
CC the Gly-Ser-Pro-PTH 1-34 peptide.
XX
SQ Sequence 111 BP; 31 A; 28 C; 25 G; 27 T; 0 U; 0 Other;

Query Match 54.2%; Score 50.4; DB 13; Length 111;
Best Local Similarity 52.2%; Pred. No. 5.2e-06;
Matches 48; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
|:|:::| ||||:| ||: |:||||:| |:||||||:|
Db 11 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 70

Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||:||||||::
Db 71 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 102

RESULT 14
ADG93260
ID ADG93260 standard; DNA; 117 BP.
XX
AC ADG93260;
XX
DT 11-MAR-2004 (first entry)
XX
DE Novel expression cassette-related PTH DNA SeqID141.
XX
KW expression cassette; high yield polypeptide production;
KW tandem polypeptide; inclusion body; gene; ds; PTH.
XX
OS Unidentified.
OS Synthetic.
XX
PN WO2003100021-A2.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-US016643.
XX
PR 24-MAY-2002; 2002US-0383370P.
XX
PA (REST-) RESTORAGEN INC.
PA (HARL/) HARLEY S.
XX
PI Harley S, Williams JA, Luan P, Xia Y;
XX
DR WPI; 2004-035128/03.
DR P-PSDB; ADG93259.
XX
PT New expression cassette comprising an operably linked nucleic acid
PT sequence, useful for producing a tandem polypeptide that forms an
PT inclusion body when expressed in a cell.
XX
PS Disclosure; SEQ ID NO 141; 157pp; English.
XX
CC This invention relates to a novel expression cassette and methods for
CC high yield production of polypeptides. The cassette comprises an operably
CC linked nucleic acid sequence, where the expression of the cassette

CC produces a tandem polypeptide that forms an inclusion body when expressed
CC in a cell. The expression cassette is useful for producing peptide and
CC polypeptide in a cell, preferably a tandem polypeptide that forms an
CC inclusion body when expressed in a cell. The present sequence is that of
CC a DNA sequence which encodes a PTH peptide which was used in the
CC exemplification of the invention.
XX
SQ Sequence 117 BP; 35 A; 27 C; 25 G; 30 T; 0 U; 0 Other;

Query Match 54.2%; Score 50.4; DB 12; Length 117;
Best Local Similarity 52.2%; Pred. No. 5.3e-06;
Matches 48; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
|:|:::| ||||:| ||: |:||||:| |:|||||:|
Db 2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:||||||||:||||||||::
Db 62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93

RESULT 15
AAT34865
ID AAT34865 standard; cDNA; 168 BP.
XX
AC AAT34865;
XX
DT 02-DEC-1996 (first entry)
XX
DE Plasmid pBN1:PTH(1-34)C-1c portion encoding PTH(1-34)Cys.
XX
KW PTH; parathyroid hormone; parathormone; C-amide; C-amidated peptide;
KW alpha-carboxamide; recombinant protein; fusion protein; transpeptidation;
KW vector; plasmid pBN1; carbonic anhydrase II; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1. .162
FT /*tag= a
FT /product= "hCA-linker-PTH(1-34)Cys fusion"
XX
PN WO9617941-A2.
XX
PD 13-JUN-1996.
XX
PF 07-DEC-1995; 95WO-US015799.
XX
PR 07-DEC-1994; 94US-00350528.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Stout JS, Patridge BE, Heriksen DB, Holmquist B, Wagner FW;
XX
DR WPI; 1996-287185/29.
DR P-PSDB; AAR98967.
XX
PT Production of C-terminal alpha-carboxamidated peptide(s) - by cleavage
PT and transpeptidation of recombinant multicopy peptide(s) or fusion
PT constructs.
XX
PS Example 7; Fig 1; 93pp; English.
XX
CC A portion (AAT34865) of plasmid pBN1:PTH(1-34)C-1c comprises DNA coding
CC for a fusion protein (AAR87867) composed of the C-terminal end of human
CC carbonic anhydrase II joined by an intraconnecting peptide (including a
CC thrombin cleavage site) to amino acids 1-34 of PTH (AAR98966), followed
CC by a Cys residue and C-terminal sequence. The complete construct can be
CC expressed in E. coli transformants. The intraconnecting peptide and C-
CC terminal Cys residue enable the recombinant protein construct to be
CC selectively reacted to produce C-terminal carboxamidated PTH(1-34)
XX
SQ Sequence 168 BP; 41 A; 44 C; 42 G; 41 T; 0 U; 0 Other;

Query Match 54.2%; Score 50.4; DB 2; Length 168;
Best Local Similarity 52.2%; Pred. No. 5.7e-06;
Matches 48; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
|:|:::| ||||:| ||: |:||||:| |:|||||:|
Db 47 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 106

Qy 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:||||||||:||||||||::
Db 107 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 138

Search completed: November 23, 2005, 23:00:15
Job time : 243.667 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:36:53 ; Search time 1823 Seconds
(without alignments)
2386.834 Million cell updates/sec

Title: US-09-475-158A-16
Perfect score: 93
Sequence: 1 gcuguuuccgaaaucggugg.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	39.2	42.2	527	1	AI909008	AI909008 QV-BT197-
	2	38.8	41.7	324	8	W19763	W19763 zb39c01.r1
	3	38.2	41.1	352	8	W39062	W39062 zb34c06.r1
	4	38.2	41.1	376	8	W38966	W38966 zb28b12.r1
	5	38.2	41.1	411	8	W37708	W37708 zc10d12.r1
	6	38.2	41.1	416	8	W31998	W31998 zb96d06.r1
	7	38.2	41.1	434	8	W38764	W38764 zb27a07.r1
	8	38.2	41.1	450	8	W56235	W56235 zc01e11.r1
	9	38.2	41.1	453	8	W33077	W33077 zc07a12.r1
	10	38.2	41.1	496	8	W56820	W56820 zc01a03.r1
	11	38.2	41.1	523	8	W52945	W52945 zc03h08.r1
	12	38.2	41.1	536	8	W19765	W19765 zb39c03.r1
	13	38.2	41.1	547	8	W52795	W52795 zc02b12.r1
	14	38.2	41.1	576	8	W56120	W56120 zc56h06.r1
	15	38.2	41.1	583	8	W39202	W39202 zb35h03.r1
c	16	38.2	41.1	595	1	AA788985	AA788985 ah29c05.s
	17	38.2	41.1	721	2	BG198564	BG198564 RST17829
c	18	38.2	41.1	741	1	AI051997	AI051997 oy29c05.x
c	19	38.2	41.1	756	1	AA843660	AA843660 ak08g07.s
	20	38.2	41.1	757	5	BX106232	BX106232 BX106232
c	21	38.2	41.1	780	1	AI028087	AI028087 ow51a12.x
	22	38.2	41.1	809	2	BG188276	BG188276 RST7292 A
	23	38.2	41.1	820	5	BX103059	BX103059 BX103059
	24	37.2	40.0	316	1	AA372113	AA372113 EST83976
c	25	36.6	39.4	575	1	AA772070	AA772070 ai41f07.s
c	26	36.6	39.4	620	6	CF231132	CF231132 PtaC0017G
c	27	36.6	39.4	766	1	AA843141	AA843141 ak06c02.s
	28	36.2	38.9	339	8	T29548	T29548 EST83988 Hu
c	29	35.8	38.5	844	6	CA184654	CA184654 SCRLST316
	30	35.6	38.3	417	9	CC894877	CC894877 ZMMBBb021
c	31	35.6	38.3	570	1	AA771739	AA771739 ai32e09.s
	32	35.4	38.1	605	7	CO984533	CO984533 GM89013B2
	33	35	37.6	540	2	BE212803	BE212803 IpBrn0085
c	34	35	37.6	705	1	AI031553	AI031553 ow48c08.x
c	35	34.8	37.4	301	11	CR159040	CR159040 Forward s
c	36	34.8	37.4	939	10	CG442723	CG442723 OGTAU17TV
	37	34.6	37.2	972	10	CNS02QMI	AL209475 Tetraodon
c	38	34.6	37.2	1013	10	CW921961	CW921961 EDCAP72TR
c	39	34.4	37.0	501	2	BE360066	BE360066 DG1_61_G0
	40	34.2	36.8	514	9	BZ137695	BZ137695 CH230-432
c	41	34.2	36.8	744	7	CK481107	CK481107 AGENCOURT
	42	34	36.6	550	5	BQ987803	BQ987803 QGF13D16.
	43	34	36.6	562	5	BU005353	BU005353 QGG7N20.y
	44	34	36.6	605	5	BQ861241	BQ861241 QGC17O20.
	45	34	36.6	650	5	BU008102	BU008102 QGH6I04.y

ALIGNMENTS

RESULT 1
AI909008
LOCUS AI909008 527 bp mRNA linear EST 30-MAR-2000
DEFINITION QV-BT197-050499-038 BT197 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI909008
VERSION AI909008.1 GI:6499688
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 527)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?t1=QV&t2=QV-BT197-038.html&t3=050499&t4=1)
Seq primer: puc 18 forward.
FEATURES Location/Qualifiers
source 1. .527
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="Adult"
/clone_lib="BT197"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 42.2%; Score 39.2; DB 1; Length 527;
Best Local Similarity 72.7%; Pred. No. 0.32;
Matches 32; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

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Qy         43 CUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCA 86
              |:||||:| |:|||||:|: |||:|||:|||:|||||||:| |
Db          2 CTGAACTCTATGGAACGTGTAGAATGGCTGCGTAAAAAACTGGA 45
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RESULT 2
W19763
LOCUS W19763 324 bp mRNA linear EST 03-MAY-1996
DEFINITION zb39c01.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305952 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W19763
VERSION W19763.1 GI:1295880
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 222.
FEATURES Location/Qualifiers
source 1. .324
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249362"
/db_xref="taxon:9606"
/clone="IMAGE:305952"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
ORIGIN

Query Match 41.7%; Score 38.8; DB 8; Length 324;
Best Local Similarity 64.7%; Pred. No. 0.4;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:|||  | |: |||:|||:|||:|| || |:|||||| |:
Db        100 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAANCTGCAGGATGT 150
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RESULT 3
W39062
LOCUS W39062 352 bp mRNA linear EST 15-MAY-1996
DEFINITION zb34c06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305482 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W39062
VERSION W39062.1 GI:1320771
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 352)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 286.
FEATURES Location/Qualifiers
source 1. .352
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248892"
/db_xref="taxon:9606"
/clone="IMAGE:305482"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
ORIGIN

Query Match 41.1%; Score 38.2; DB 8; Length 352;
Best Local Similarity 64.7%; Pred. No. 0.61;

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  Matches   33;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:|||  | |: |||:|||:|||:|| || |:|||||| |:
Db        225 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 275


RESULT 4
W38966
LOCUS       W38966                   376 bp    mRNA    linear   EST 15-MAY-1996
DEFINITION  zb28b12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:304895 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W38966
VERSION     W38966.1  GI:1320674
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET.
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1248305"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:304895"
                     /tissue_type="parathyroid tumor"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_parathyroid_tumor_NbHPA"
                     /note="Organ: parathyroid gland; Vector: pT7T3D
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTT
                     TTTTT-3'], double-stranded cDNA was size selected, ligated
                     to Eco RI adapters (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of a modified pT7T3
                     vector (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                     adenomas was kindly provided by Dr. Stephen Marx, National
                     Institute of Diabetes and Digestive and Kidney Diseases,
                     NIH."
ORIGIN

  Query Match             41.1%;  Score 38.2;  DB 8;  Length 376;
  Best Local Similarity   64.7%;  Pred. No. 0.62;
  Matches   33;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:|||  | |: |||:|||:|||:|| || |:|||||| |:
Db        212 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 262


RESULT 5
W37708
LOCUS       W37708                   411 bp    mRNA    linear   EST 10-OCT-1996
DEFINITION  zc10d12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:321911 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W37708
VERSION     W37708.1  GI:1319302
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 876   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 396.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1259569"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:321911"
                     /tissue_type="parathyroid tumor"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_parathyroid_tumor_NbHPA"
                     /note="Organ: parathyroid gland; Vector: pT7T3D
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTT
                     TTTTT-3'], double-stranded cDNA was size selected, ligated
                     to Eco RI adapters (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of a modified pT7T3
                     vector (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                     adenomas was kindly provided by Dr. Stephen Marx, National
                     Institute of Diabetes and Digestive and Kidney Diseases,
                     NIH."
ORIGIN

  Query Match             41.1%;  Score 38.2;  DB 8;  Length 411;
  Best Local Similarity   64.7%;  Pred. No. 0.63;
  Matches   33;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:|||  | |: |||:|||:|||:|| || |:|||||| |:
Db        250 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 300


RESULT 6
W31998
LOCUS       W31998                   416 bp    mRNA    linear   EST 20-AUG-1996
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DEFINITION  zb96d06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:320651 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W31998
VERSION     W31998.1  GI:1313010
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 416)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
            Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
            and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
   PUBMED   8889549
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 771   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 386.
FEATURES             Location/Qualifiers
     source          1. .416
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1258309"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:320651"
                     /tissue_type="parathyroid tumor"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_parathyroid_tumor_NbHPA"
                     /note="Organ: parathyroid gland; Vector: pT7T3D
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT
                     TTTTT-3'], double-stranded cDNA was size selected, ligated
                     to Eco RI adapters (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of a modified pT7T3
                     vector (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                     adenomas was kindly provided by Dr. Stephen Marx, National
                     Institute of Diabetes and Digestive and Kidney Diseases,
                     NIH."
ORIGIN

  Query Match             41.1%;  Score 38.2;  DB 8;  Length 416;
  Best Local Similarity   64.7%;  Pred. No. 0.63;
  Matches   33;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:||| | |: |||:|||:|||:|| || |:|||||| |:
Db         74 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 124


RESULT 7
W38764
LOCUS       W38764                   434 bp    mRNA    linear   EST 15-MAY-1996
DEFINITION  zb27a07.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:304788 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W38764
VERSION     W38764.1  GI:1320471
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 434)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET
            High quality sequence stop: 253.
FEATURES             Location/Qualifiers
     source          1. .434
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1248198"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:304788"
                     /tissue_type="parathyroid tumor"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_parathyroid_tumor_NbHPA"
                     /note="Organ: parathyroid gland; Vector: pT7T3D
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT
                     TTTTT-3'], double-stranded cDNA was size selected, ligated
                     to Eco RI adapters (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of a modified pT7T3
                     vector (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                     adenomas was kindly provided by Dr. Stephen Marx, National
                     Institute of Diabetes and Digestive and Kidney Diseases,
                     NIH."
ORIGIN

  Query Match             41.1%;  Score 38.2;  DB 8;  Length 434;
  Best Local Similarity   64.7%;  Pred. No. 0.63;
  Matches   33;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:||| | |: |||:|||:|||:|| || |:|||||| |:
Db        214 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 264


RESULT 8
W56235
LOCUS       W56235                   450 bp    mRNA    linear   EST 10-OCT-1996
DEFINITION  zc01e11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:321068 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W56235
VERSION     W56235.1  GI:1358124
KEYWORDS    EST.
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 865   Std Error: 0.00
            Seq primer: mob.REGA+ET.
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1258726"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:321068"
                     /tissue_type="parathyroid tumor"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_parathyroid_tumor_NbHPA"
                     /note="Organ: parathyroid gland; Vector: pT7T3D
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT
                     TTTTT-3'], double-stranded cDNA was size selected, ligated
                     to Eco RI adapters (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of a modified pT7T3
                     vector (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                     adenomas was kindly provided by Dr. Stephen Marx, National
                     Institute of Diabetes and Digestive and Kidney Diseases,
                     NIH."
ORIGIN

  Query Match             41.1%;  Score 38.2;  DB 8;  Length 450;
  Best Local Similarity   64.7%;  Pred. No. 0.63;
  Matches   33;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:||| | |: |||:|||:|||:|| || |:|||||| |:
Db        229 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 279


RESULT 9
W33077
LOCUS       W33077                   453 bp    mRNA    linear   EST 10-OCT-1996
DEFINITION  zc07a12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:321598 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W33077
VERSION     W33077.1  GI:1315062
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 453)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 871   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 367.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="GDB:1259256"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:321598"
                     /tissue_type="parathyroid tumor"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_parathyroid_tumor_NbHPA"
                     /note="Organ: parathyroid gland; Vector: pT7T3D
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT
                     TTTTT-3'], double-stranded cDNA was size selected, ligated
                     to Eco RI adapters (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of a modified pT7T3
                     vector (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                     adenomas was kindly provided by Dr. Stephen Marx, National
                     Institute of Diabetes and Digestive and Kidney Diseases,
                     NIH."
ORIGIN

  Query Match             41.1%;  Score 38.2;  DB 8;  Length 453;
  Best Local Similarity   64.7%;  Pred. No. 0.63;
  Matches   33;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:||| | |: |||:|||:|||:|| || |:|||||| |:
Db        241 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 291


RESULT 10
W56820
LOCUS       W56820                   496 bp    mRNA    linear   EST 10-OCT-1996
DEFINITION  zc01a03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:321004 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W56820
VERSION     W56820.1  GI:1358743
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 496)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
```

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 858 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 424.
FEATURES Location/Qualifiers
source 1. .496
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258662"
/db_xref="taxon:9606"
/clone="IMAGE:321004"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
ORIGIN

Query Match 41.1%; Score 38.2; DB 8; Length 496;
Best Local Similarity 64.7%; Pred. No. 0.64;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
:|:||||:| |:||| | |: |||:|||:|||:|| || |:|||||| |:
Db 219 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 269

RESULT 11
W52945
LOCUS W52945 523 bp mRNA linear EST 10-OCT-1996
DEFINITION zc03h08.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321279 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W52945
VERSION W52945.1 GI:1350379
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 523)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 702 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 304.
FEATURES Location/Qualifiers
source 1. .523
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258937"
/db_xref="taxon:9606"
/clone="IMAGE:321279"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
ORIGIN

Query Match 41.1%; Score 38.2; DB 8; Length 523;
Best Local Similarity 64.7%; Pred. No. 0.65;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
:|:||||:| |:||| | |: |||:|||:|||:|| || |:|||||| |:
Db 39 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 89

RESULT 12
W19765
LOCUS W19765 536 bp mRNA linear EST 03-MAY-1996
DEFINITION zb39c03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305956 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W19765
VERSION W19765.1 GI:1295882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 536)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

```
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET
            High quality sequence stop: 352.
FEATURES              Location/Qualifiers
     source           1. .536
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
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                      /clone_lib="Soares_parathyroid_tumor_NbHPA"
                      /note="Organ: parathyroid gland; Vector: pT7T3D
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                      oligo(dT) primer
                      [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT
                      TTTTT-3'], double-stranded cDNA was size selected, ligated
                      to Eco RI adapters (Pharmacia), digested with Not I and
                      cloned into the Not I and Eco RI sites of a modified pT7T3
                      vector (Pharmacia). Library went through one round of
                      normalization to a Cot = 5. Library constructed by Bento
                      Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                      adenomas was kindly provided by Dr. Stephen Marx, National
                      Institute of Diabetes and Digestive and Kidney Diseases,
                      NIH."
ORIGIN

  Query Match             41.1%;  Score 38.2;  DB 8;  Length 536;
  Best Local Similarity   64.7%;  Pred. No. 0.65;
  Matches   33;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:|||  | |: |||:|||:|||:|| || |:|||||| |:
Db        229 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 279


RESULT 13
W52795
LOCUS       W52795                   547 bp    mRNA    linear   EST 10-OCT-1996
DEFINITION  zc02b12.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:321119 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W52795
VERSION     W52795.1  GI:1350435
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 651   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 403.
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     source           1. .547
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                      /dev_stage="adult"
                      /lab_host="DH10B (ampicillin resistant)"
                      /clone_lib="Soares_parathyroid_tumor_NbHPA"
                      /note="Organ: parathyroid gland; Vector: pT7T3D
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                      oligo(dT) primer
                      [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTT
                      TTTTT-3'], double-stranded cDNA was size selected, ligated
                      to Eco RI adapters (Pharmacia), digested with Not I and
                      cloned into the Not I and Eco RI sites of a modified pT7T3
                      vector (Pharmacia). Library went through one round of
                      normalization to a Cot = 5. Library constructed by Bento
                      Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
                      adenomas was kindly provided by Dr. Stephen Marx, National
                      Institute of Diabetes and Digestive and Kidney Diseases,
                      NIH."
ORIGIN

  Query Match             41.1%;  Score 38.2;  DB 8;  Length 547;
  Best Local Similarity   64.7%;  Pred. No. 0.65;
  Matches   33;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:|||  | |: |||:|||:|||:|| || |:|||||| |:
Db         18 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 68


RESULT 14
W56120
LOCUS       W56120                   576 bp    mRNA    linear   EST 11-OCT-1996
DEFINITION  zc56h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            IMAGE:326363 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   W56120
VERSION     W56120.1  GI:1358009
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 576)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 904   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 433.
FEATURES              Location/Qualifiers
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/organism="Homo sapiens"
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/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 41.1%; Score 38.2; DB 8; Length 576;
Best Local Similarity 64.7%; Pred. No. 0.66;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              :|:||||:| |:|||  | |: |||:|||:|||:|| || |:|||||| |:
Db        224 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 274
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RESULT 15
W39202
LOCUS W39202 583 bp mRNA linear EST 15-MAY-1996
DEFINITION zb35h03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305621 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION W39202
VERSION W39202.1 GI:1320911
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 400.
FEATURES Location/Qualifiers
source 1. .583
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/clone="IMAGE:305621"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

Query Match 41.1%; Score 38.2; DB 8; Length 583;
Best Local Similarity 64.7%; Pred. No. 0.66;
Matches 33; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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Db         93 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 143
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Search completed: November 24, 2005, 01:30:31
Job time : 1825 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 22:44:43 ; Search time 73.6667 Seconds
(without alignments)
2244.071 Million cell updates/sec

Title: US-09-475-158A-16
Perfect score: 93
Sequence: 1 gcuguuuccgaaaucggugg.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53.6	57.6	258	3	US-09-463-282D-26	Sequence 26, Appl
c 2	48.4	52.0	74	2	US-08-142-551B-132	Sequence 132, App
3	46.2	49.7	141	2	US-08-468-275-3	Sequence 3, Appli
c 4	46.2	49.7	141	2	US-08-468-275-5	Sequence 5, Appli
5	46.2	49.7	141	3	US-09-007-466-3	Sequence 3, Appli
c 6	46.2	49.7	141	3	US-09-007-466-5	Sequence 5, Appli
7	46.2	49.7	141	3	US-08-952-980B-3	Sequence 3, Appli
c 8	46.2	49.7	141	3	US-08-952-980B-5	Sequence 5, Appli
9	46.2	49.7	207	2	US-08-142-551B-8	Sequence 8, Appli
10	43.4	46.7	45	3	US-09-463-282D-5	Sequence 5, Appli
11	43	46.2	67	3	US-09-068-738A-9	Sequence 9, Appli
12	39.8	42.8	102	3	US-10-340-484-14	Sequence 14, Appl
13	39.8	42.8	234	2	US-08-733-446-19	Sequence 19, Appl
14	39.8	42.8	234	2	US-08-733-446-61	Sequence 61, Appl
15	39.8	42.8	237	2	US-08-733-446-20	Sequence 20, Appl
16	39.8	42.8	240	2	US-08-733-446-21	Sequence 21, Appl
17	39.8	42.8	243	2	US-08-733-446-22	Sequence 22, Appl
18	39.8	42.8	245	2	US-08-733-446-24	Sequence 24, Appl
c 19	39.8	42.8	247	2	US-08-733-446-25	Sequence 25, Appl
20	39.8	42.8	248	2	US-08-733-446-26	Sequence 26, Appl
c 21	39.8	42.8	250	2	US-08-733-446-27	Sequence 27, Appl
22	39.8	42.8	251	2	US-08-733-446-28	Sequence 28, Appl
23	39.8	42.8	252	2	US-08-689-190-1	Sequence 1, Appli
24	39.8	42.8	252	2	US-08-733-446-23	Sequence 23, Appl
25	39.8	42.8	252	2	US-08-733-446-56	Sequence 56, Appl
26	39.8	42.8	252	2	US-08-733-446-58	Sequence 58, Appl
27	39.8	42.8	252	2	US-08-835-231-34	Sequence 34, Appl
28	39.8	42.8	252	3	US-09-108-661-34	Sequence 34, Appl
c 29	39.8	42.8	253	2	US-08-733-446-29	Sequence 29, Appl
30	39.8	42.8	254	2	US-08-733-446-30	Sequence 30, Appl
c 31	39.8	42.8	256	2	US-08-733-446-31	Sequence 31, Appl
32	39.8	42.8	263	2	US-08-689-190-3	Sequence 3, Appli
33	39.8	42.8	263	2	US-08-733-446-32	Sequence 32, Appl
c 34	39.8	42.8	265	2	US-08-689-190-4	Sequence 4, Appli
c 35	39.8	42.8	265	2	US-08-733-446-33	Sequence 33, Appl
36	38.2	41.1	252	2	US-07-863-014-1	Sequence 1, Appli
37	38.2	41.1	252	2	US-08-332-453-1	Sequence 1, Appli
38	38.2	41.1	537	2	US-08-835-231-5	Sequence 5, Appli
39	38.2	41.1	537	2	US-08-835-231-6	Sequence 6, Appli
40	38.2	41.1	537	3	US-09-108-661-5	Sequence 5, Appli
41	38.2	41.1	537	3	US-09-108-661-6	Sequence 6, Appli
c 42	38.2	41.1	601	3	US-09-949-016-18519	Sequence 18519, A
c 43	38.2	41.1	601	3	US-09-949-016-66782	Sequence 66782, A
44	38.2	41.1	772	3	US-09-949-016-51	Sequence 51, Appl
45	38.2	41.1	773	3	US-09-949-016-1970	Sequence 1970, Ap

ALIGNMENTS

RESULT 1
US-09-463-282D-26
; Sequence 26, Application US/09463282D
; Patent No. 6500647
; GENERAL INFORMATION:
; APPLICANT: Jung, Eun-Kyung
; APPLICANT: Park, Doo-Hong
; APPLICANT: Chung, Soo Il
; TITLE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE
; FILE REFERENCE: 0136/0G626
; CURRENT APPLICATION NUMBER: US/09/463,282D
; CURRENT FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: PCT/KR98/00146
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: KR 1997-35230
; PRIOR FILING DATE: 1997-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-463-282D-26

Query Match 57.6%; Score 53.6; DB 3; Length 258;
Best Local Similarity 51.1%; Pred. No. 3e-07;
Matches 47; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
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Db          2 CTGTTTCGGAAATCCAGCTTATGCATAACCTGGGTAAACATCTGAACTCGATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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RESULT 2
US-08-142-551B-132/c
; Sequence 132, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  132:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  74 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-142-551B-132

  Query Match             52.0%;  Score 48.4;  DB 2;  Length 74;
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RESULT 3
US-08-468-275-3
; Sequence 3, Application US/08468275
; Patent No. 5747453
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,275
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..138
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  25
US-08-468-275-3

  Query Match             49.7%;  Score 46.2;  DB 2;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 4.8e-05;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                  ||:      |:||||:|| : || ||:|
Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 4
US-08-468-275-5/c
; Sequence 5, Application US/08468275
; Patent No. 5747453
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,275
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-468-275-5

  Query Match             49.7%;  Score 46.2;  DB 2;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 4.8e-05;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

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Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 5
US-09-007-466-3
; Sequence 3, Application US/09007466
; Patent No. 6313092
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/007,466
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/468,275
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  0360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..138
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  25
US-09-007-466-3

  Query Match             49.7%;  Score 46.2;  DB 3;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 4.8e-05;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                  ||:      |:||||:|| : || ||:|
Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 6
US-09-007-466-5/c
; Sequence 5, Application US/09007466
; Patent No. 6313092
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/007,466
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/468,275
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  0360-0002; ARC-2349
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 496-8150
;      TELEFAX:  (415) 496-8048
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-007-466-5

  Query Match             49.7%;  Score 46.2;  DB 3;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 4.8e-05;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                  ||:      |:||||:|| : || ||:|
Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 7
US-08-952-980B-3
; Sequence 3, Application US/08952980B
; Patent No. 6333189
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;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/952,980B
;      FILING DATE:  20-NOV-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  2349 CIP 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 496-8150
;      TELEFAX:  (650) 496-8048
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..138
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  25
US-08-952-980B-3

  Query Match             49.7%;  Score 46.2;  DB 3;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 4.8e-05;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                ||:      |:||||:|| : || ||:|
Db         26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db         86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116


RESULT 8
US-08-952-980B-5/c
; Sequence 5, Application US/08952980B
; Patent No. 6333189
;  GENERAL INFORMATION:
;    APPLICANT:  HOLLADAY, LESLIE A.
;    APPLICANT:  OLDENBURG, KEVIN R.
;    TITLE OF INVENTION:  METHOD FOR INCREASING THE
;    TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALZA CORPORATION
;      STREET:  950 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94303-0802
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/952,980B
;      FILING DATE:  20-NOV-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLER, D. BYRON
;      REGISTRATION NUMBER:  30,661
;      REFERENCE/DOCKET NUMBER:  2349 CIP 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 496-8150
;      TELEFAX:  (650) 496-8048
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-952-980B-5

  Query Match             49.7%;  Score 46.2;  DB 3;  Length 141;
  Best Local Similarity   51.6%;  Pred. No. 4.8e-05;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::||||||:|                ||:      |:||||:|| : || ||:|
Db        116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 57

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db         56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26


RESULT 9
US-08-142-551B-8
; Sequence 8, Application US/08142551B
; Patent No. 5814603
;  GENERAL INFORMATION:
;    APPLICANT:  Oldenburg, Kevin R.
;    APPLICANT:  Selick, Harold E.
;    TITLE OF INVENTION:  COMPOUNDS WITH PTH ACTIVITY AND
;    TITLE OF INVENTION:  RECOMBINANT DNA VECTORS ENCODING SAME
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22313
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/142,551B
;      FILING DATE:  25-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/077,296
;      FILING DATE:  14-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/898,219
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/965,677
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;      FILING DATE:  22-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Swiss, Gerald F.
;      REGISTRATION NUMBER:  30,113
;      REFERENCE/DOCKET NUMBER:  000324-010
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-7400
;      TELEFAX:  (415) 854-8275
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  207 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..201
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..51
;      OTHER INFORMATION:  /note= "Encodes the leader peptide
;      OTHER INFORMATION:  sequence that serves to direct the protein into
;      OTHER INFORMATION:  inclusion bodies."
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  70..174
;      OTHER INFORMATION:  /note= "Encodes the protein or
;      OTHER INFORMATION:  peptide of interest"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  175..207
;      OTHER INFORMATION:  /note= "Encodes amino acid sequence
;      OTHER INFORMATION:  having six histamines that serves as a tag for the
;      OTHER INFORMATION:  purification of the protein on a nickel column."
US-08-142-551B-8

  Query Match             49.7%;  Score 46.2;  DB 2;  Length 207;
  Best Local Similarity   51.6%;  Pred. No. 5.3e-05;
  Matches   47;  Conservative   16;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              | |:::|||||||:|                   ||:      |:||||:|| : || ||:|
Db         71 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 130

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGU 92
              ::|||:|||:|||:|||||||:||||||||:
Db        131 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 161


RESULT 10
US-09-463-282D-5
; Sequence 5, Application US/09463282D
; Patent No. 6500647
; GENERAL INFORMATION:
;  APPLICANT: Jung, Eun-Kyung
;  APPLICANT:  Park, Doo-Hong
;  APPLICANT:  Chung, Soo Il
;  TITLE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE
;  FILE REFERENCE: 0136/0G626
;  CURRENT APPLICATION NUMBER: US/09/463,282D
;  CURRENT FILING DATE:  2000-01-20
;  PRIOR APPLICATION NUMBER: PCT/KR98/00146
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: KR 1997-35230
;  PRIOR FILING DATE: 1997-07-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-463-282D-5

  Query Match             46.7%;  Score 43.4;  DB 3;  Length 45;
  Best Local Similarity   73.3%;  Pred. No. 0.00027;
  Matches   33;  Conservative   11;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCA 86
              :|:||||:| |:||||||:|::|||:|||:|||:||||||||:|||
Db          1 TCTGAACTCGATGGAACGTGTTGAATGGCTGCGTAAAAAACTGCA 45


RESULT 11
US-09-068-738A-9
; Sequence 9, Application US/09068738A
; Patent No. 6136564
;  GENERAL INFORMATION:
;    APPLICANT:  KOPETZKI, Erhard
;    TITLE OF INVENTION:  PROCESS FOR THE PREPARATION OF PEPTIDES VIA
;    TITLE OF INVENTION:  STREPTAVIDIN FUSION PROTEINS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARENT FOX KINTNER PLOTKIN & KAHN
;      STREET:  1050 CONNECTICUT AVENUE, NW, SUITE 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20036-5339
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/068,738A
;      FILING DATE:  June 25, 1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP 96/04850
;      FILING DATE:  11-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berman, Richard J.
;      REGISTRATION NUMBER:  39,107
;      REFERENCE/DOCKET NUMBER:  P108341-08035
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  67 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "synthetic
;      DESCRIPTION:  oligonucleotide"
US-09-068-738A-9

  Query Match             46.2%;  Score 43;  DB 3;  Length 67;
  Best Local Similarity   76.7%;  Pred. No. 0.00039;
  Matches   33;  Conservative   10;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 CAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ||:||||||:|::|||:|||:|||:|||||||:||||||::
Db          1 CATGGAACGTGTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 43


RESULT 12
US-10-340-484-14
; Sequence 14, Application US/10340484
; Patent No. 6875739
; GENERAL INFORMATION:
;  APPLICANT: Stewart, Andrew F.
;  TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
;  TITLE OF INVENTION:  Drugs
;  FILE REFERENCE: 25200-501
;  CURRENT APPLICATION NUMBER: US/10/340,484
;  CURRENT FILING DATE:  2003-01-10
;  PRIOR APPLICATION NUMBER: 60/347,215
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;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: 60/353,296
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: 60/368,955
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: 60/379,125
;  PRIOR FILING DATE: 2002-05-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 102
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-340-484-14

  Query Match             42.8%;  Score 39.8;  DB 3;  Length 102;
  Best Local Similarity   64.7%;  Pred. No. 0.0041;
  Matches   33;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : :||||:|||:||| ||:|: |||:|||:|||:|| ||  :|||||| |:
Db         42 TTTGAACTCCATGGAGCGTGTAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92


RESULT 13
US-08-733-446-19
; Sequence 19, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  234 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..234
;      IDENTIFICATION METHOD:  E
US-08-733-446-19

  Query Match             42.8%;  Score 39.8;  DB 2;  Length 234;
  Best Local Similarity   64.7%;  Pred. No. 0.0049;
  Matches   33;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : :||||:|||:||| ||:|: |||:|||:|||:|| ||  :|||||| |:
Db         24 TTTGAACTCCATGGAGCGTGTAGAATGGCTGCGTAAGAAGTTGCAGGATGT 74


RESULT 14
US-08-733-446-61
; Sequence 61, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  234 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..234
;      NAME/KEY:  mutation
;      LOCATION:  4,6
;      IDENTIFICATION METHOD:  E
US-08-733-446-61

  Query Match             42.8%;  Score 39.8;  DB 2;  Length 234;
  Best Local Similarity   64.7%;  Pred. No. 0.0049;
  Matches   33;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : :||||:|||:||| ||:|: |||:|||:|||:|| ||  :|||||| |:
Db         24 TTTGAACTCCATGGAGCGTGTAGAATGGCTGCGTAAGAAGTTGCAGGATGT 74
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```
RESULT 15
US-08-733-446-20
; Sequence 20, Application US/08733446
; Patent No. 5856138
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUDA, Tsunehiko
;    TITLE OF INVENTION:  HUMAN PARATHYROID HORMONE MUTEINS AND
;    TITLE OF INVENTION:  PRODUCTION THEREOF
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/733,446
;      FILING DATE:  18-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/402,970
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/926,787
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEUNER, George W
;      REGISTRATION NUMBER:  26964
;      REFERENCE/DOCKET NUMBER:  42025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)523-3400
;      TELEFAX:  (617)523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  237 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid, synthetic DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..237
;      IDENTIFICATION METHOD:  E
US-08-733-446-20

  Query Match             42.8%;  Score 39.8;  DB 2;  Length 237;
  Best Local Similarity   64.7%;  Pred. No. 0.0049;
  Matches   33;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
              : :||||:|||:||| ||:|: |||:|||:|||:|| ||  :|||||| |:
Db         27 TTTGAACTCCATGGAGCGTGTAGAATGGCTGCGTAAGAAGTTGCAGGATGT 77


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 23, 2005, 23:59:22 ; Search time 412.667 Seconds
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Title: US-09-475-158A-16
Perfect score: 93
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	55.9	489	6	US-10-117-109-14	Sequence 14, Appl
2	52	55.9	489	6	US-10-407-078-14	Sequence 14, Appl
3	52	55.9	489	6	US-10-407-078-43	Sequence 43, Appl
4	50.4	54.2	102	9	US-10-997-078-60	Sequence 60, Appl
5	50.4	54.2	102	9	US-10-997-700-33	Sequence 33, Appl
6	50.4	54.2	111	9	US-10-997-078-61	Sequence 61, Appl
7	50.4	54.2	111	9	US-10-997-700-34	Sequence 34, Appl
8	50.4	54.2	117	9	US-10-997-078-141	Sequence 141, App
9	50.4	54.2	252	9	US-10-997-078-62	Sequence 62, Appl
10	50.4	54.2	252	9	US-10-997-700-35	Sequence 35, Appl
11	50.4	54.2	264	9	US-10-997-700-89	Sequence 89, Appl
12	50.4	54.2	276	9	US-10-997-762-18	Sequence 18, Appl
13	50.4	54.2	276	9	US-10-997-822-3	Sequence 3, Appli
14	50.4	54.2	276	9	US-10-997-700-75	Sequence 75, Appl
15	50.4	54.2	282	9	US-10-997-078-133	Sequence 133, App
16	50.4	54.2	291	9	US-10-997-700-76	Sequence 76, Appl
17	50.4	54.2	291	9	US-10-997-700-77	Sequence 77, Appl
18	50.4	54.2	321	9	US-10-997-700-91	Sequence 91, Appl
19	50.4	54.2	420	9	US-10-997-700-93	Sequence 93, Appl
20	50.4	54.2	426	9	US-10-997-762-20	Sequence 20, Appl
21	44.6	48.0	717	8	US-10-848-279-7	Sequence 7, Appli
22	44.6	48.0	945	8	US-10-848-279-8	Sequence 8, Appli
23	41.4	44.5	106	3	US-09-746-945-11	Sequence 11, Appl
c 24	41.4	44.5	107	3	US-09-746-945-12	Sequence 12, Appl
25	39.8	42.8	102	6	US-10-340-484-14	Sequence 14, Appl
26	39	41.9	51	3	US-09-879-257A-51	Sequence 51, Appl
c 27	39	41.9	51	3	US-09-879-257A-52	Sequence 52, Appl
28	38.4	41.3	348	6	US-10-437-038-1	Sequence 1, Appli
29	38.4	41.3	348	6	US-10-359-091-1	Sequence 1, Appli
30	38.4	41.3	432	6	US-10-437-038-3	Sequence 3, Appli
31	38.4	41.3	432	6	US-10-359-091-3	Sequence 3, Appli
32	38.4	41.3	874	6	US-10-437-038-7	Sequence 7, Appli
33	38.4	41.3	874	6	US-10-359-091-7	Sequence 7, Appli
34	38.2	41.1	102	9	US-10-775-204-24	Sequence 24, Appl
35	38.2	41.1	102	9	US-10-775-204-25	Sequence 25, Appl
36	38.2	41.1	102	9	US-10-775-204-51	Sequence 51, Appl
37	38.2	41.1	102	9	US-10-775-204-52	Sequence 52, Appl
38	38.2	41.1	102	9	US-10-775-204-57	Sequence 57, Appl
39	38.2	41.1	102	9	US-10-775-204-60	Sequence 60, Appl
40	38.2	41.1	102	9	US-10-775-204-61	Sequence 61, Appl
41	38.2	41.1	102	9	US-10-775-204-64	Sequence 64, Appl
42	38.2	41.1	102	9	US-10-775-204-69	Sequence 69, Appl
43	38.2	41.1	102	9	US-10-775-204-72	Sequence 72, Appl
44	38.2	41.1	102	9	US-10-775-204-1434	Sequence 1434, Ap
45	38.2	41.1	102	9	US-10-775-204-1435	Sequence 1435, Ap

ALIGNMENTS

RESULT 1
US-10-117-109-14
; Sequence 14, Application US/10117109
; Publication No. US20030191056A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; APPLICANT: Walker, Kenneth
; APPLICANT: Xiong, Fei
; TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the Serü
; FILE REFERENCE: A-813
; CURRENT APPLICATION NUMBER: US/10/117,109
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-117-109-14

Query Match 55.9%; Score 52; DB 6; Length 489;
Best Local Similarity 51.1%; Pred. No. 2.6e-07;
Matches 47; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|           :      ||:     :|:||||:| |:|||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGTAAACATCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|| ||||:||||||::
Db         65 TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96
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RESULT 2
US-10-407-078-14
; Sequence 14, Application US/10407078
; Publication No. US20030195154A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Kenneth
; APPLICANT: Xiong, Fei
; TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the Serü
; FILE REFERENCE: A-813A
; CURRENT APPLICATION NUMBER: US/10/407,078
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: A-813
; PRIOR FILING DATE: 2002-04-04

```
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 489
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-407-078-14

  Query Match             55.9%;  Score 52;  DB 6;  Length 489;
  Best Local Similarity   51.1%;  Pred. No. 2.6e-07;
  Matches   47;  Conservative   20;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|           :      ||:     :|:||||:| |:|||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGTAAACATCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|| ||||:||||||::
Db         65 TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96


RESULT 3
US-10-407-078-43
; Sequence 43, Application US/10407078
; Publication No. US20030195154A1
; GENERAL INFORMATION:
;  APPLICANT: Walker, Kenneth
;  APPLICANT:  Xiong, Fei
;  TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the Seru
;  FILE REFERENCE: A-813A
;  CURRENT APPLICATION NUMBER: US/10/407,078
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: A-813
;  PRIOR FILING DATE: 2002-04-04
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 489
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-407-078-43

  Query Match             55.9%;  Score 52;  DB 6;  Length 489;
  Best Local Similarity   51.1%;  Pred. No. 2.6e-07;
  Matches   47;  Conservative   20;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|           :      ||:     :|:||||:| |:|||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGTAAACATCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|| ||||:||||||::
Db         65 TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96


RESULT 4
US-10-997-078-60
; Sequence 60, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
;   LENGTH: 102
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-34).
US-10-997-078-60

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 102;
  Best Local Similarity   52.2%;  Pred. No. 6.2e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                     ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:|||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 5
US-10-997-700-33
; Sequence 33, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 102
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-34).
US-10-997-700-33

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 102;
  Best Local Similarity   52.2%;  Pred. No. 6.2e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                     ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:|||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 6
US-10-997-078-61
; Sequence 61, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
;  FILE REFERENCE: 1627.010US1
```

```
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 111
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-37).
US-10-997-078-61

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 111;
  Best Local Similarity   52.2%;  Pred. No. 6.3e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                    ||:      |:||||:| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 7
US-10-997-700-34
; Sequence 34, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 111
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-37).
US-10-997-700-34

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 111;
  Best Local Similarity   52.2%;  Pred. No. 6.3e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                    ||:      |:||||:| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 8
US-10-997-078-141
; Sequence 141, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptid
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
;   LENGTH: 117
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PTH sequence.
US-10-997-078-141

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 117;
  Best Local Similarity   52.2%;  Pred. No. 6.4e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                    ||:      |:||||:| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 9
US-10-997-078-62
; Sequence 62, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
;   LENGTH: 252
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-84).
US-10-997-078-62

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 252;
  Best Local Similarity   52.2%;  Pred. No. 7.6e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                    ||:      |:||||:| |:||||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
```

```
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 10
US-10-997-700-35
; Sequence 35, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 252
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: PTH(1-84).
US-10-997-700-35

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 252;
  Best Local Similarity   52.2%;  Pred. No. 7.6e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:|||||:|
Db          2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 61

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93


RESULT 11
US-10-997-700-89
; Sequence 89, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
;   LENGTH: 264
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic pBN121-M-PTH(1-84).
US-10-997-700-89

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 264;
  Best Local Similarity   52.2%;  Pred. No. 7.7e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:|||||:|
Db          5 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 64

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         65 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 96


RESULT 12
US-10-997-762-18
; Sequence 18, Application US/10997762
; Publication No. US20050227313A1
; GENERAL INFORMATION:
;  APPLICANT: Seo, Jin Seog
;  APPLICANT:  Strydom, Daniel
;  APPLICANT:  Holmquist, Barton
;  APPLICANT:  Restoragen Inc.
;  TITLE OF INVENTION: Polypeptide Cleavage Process
;  FILE REFERENCE: 1627.026US1
;  CURRENT APPLICATION NUMBER: US/10/997,762
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16468
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,488
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 276
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence of a chimeric synthetic protein
US-10-997-762-18

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 276;
  Best Local Similarity   52.2%;  Pred. No. 7.8e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:|||||:|
Db        173 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 232

Qy         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264


RESULT 13
US-10-997-822-3
; Sequence 3, Application US/10997822
; Publication No. US20050227314A1
; GENERAL INFORMATION:
;  APPLICANT: Holmquist, B.
;  APPLICANT:  Strydom, D.
;  APPLICANT:  Gensalk, X.
;  APPLICANT:  Cryer, R.
;  TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
;  FILE REFERENCE: 1627.011US1
;  CURRENT APPLICATION NUMBER: US/10/997,822
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16647
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,484
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 276
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleotide sequence of a synthetic chimeric protein.
US-10-997-822-3
```

```
  Query Match             54.2%;  Score 50.4;  DB 9;  Length 276;
  Best Local Similarity   52.2%;  Pred. No. 7.8e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:||||||:|
Db        173 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 232

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264


RESULT 14
US-10-997-700-75
; Sequence 75, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.009US1
;  CURRENT APPLICATION NUMBER: US/10/997,700
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: US 60/383,212
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
;   LENGTH: 276
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic PCR product.
US-10-997-700-75

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 276;
  Best Local Similarity   52.2%;  Pred. No. 7.8e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:||||||:|
Db         14 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 73

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db         74 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 105


RESULT 15
US-10-997-078-133
; Sequence 133, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
;  APPLICANT: Wagner, F.
;  APPLICANT:  Peng, L.
;  APPLICANT:  Xia, U.
;  APPLICANT:  Holmquist, B.
;  APPLICANT:  Restoragen, Inc.
;  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti
;  FILE REFERENCE: 1627.010US1
;  CURRENT APPLICATION NUMBER: US/10/997,078
;  CURRENT FILING DATE:  2004-11-24
;  PRIOR APPLICATION NUMBER: PCT/US03/16643
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 60/383,370
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
;   LENGTH: 282
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A synthetic sequence for the T7tagVg-PTH(1-34) cassette.
US-10-997-078-133

  Query Match             54.2%;  Score 50.4;  DB 9;  Length 282;
  Best Local Similarity   52.2%;  Pred. No. 7.8e-07;
  Matches   48;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
              |:|:::| ||||:|                  ||:      |:||||:| |:||||||:|
Db        167 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 226

Qy         62 UUGAAUGGCUGCGUAAAAAAACUGCAGGACGUU 93
              ::|||:|||:|||:|||||||:||||||::
Db        227 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 258


Search completed: November 24, 2005, 04:46:56
Job time : 412.667 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 24, 2005, 01:30:39 ; Search time 195 Seconds
(without alignments)
70.875 Million cell updates/sec

Title: US-09-475-158A-16
Perfect score: 93
Sequence: 1 gcuguuuccgaaaucggugg.....guaaaaaacugcaggacguu 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3205263 seqs, 74304013 residues

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	28.2	30.3	947	1	US-10-927-641-116	Sequence 116, App
c	2	28.2	30.3	3507	1	US-10-509-422-1	Sequence 1, Appli
c	3	28.2	30.3	3704	1	US-10-509-422-3	Sequence 3, Appli
	4	28	30.1	6497	1	US-10-821-234-839	Sequence 839, App
c	5	26.4	28.4	3371	1	US-10-131-826A-35	Sequence 35, Appl
c	6	25.2	27.1	2536	1	US-10-793-626-4301	Sequence 4301, Ap
c	7	25	26.9	1065	1	US-10-821-234-766	Sequence 766, App
c	8	24.6	26.5	2218	1	US-10-821-234-119	Sequence 119, App
c	9	24.4	26.2	2043	1	US-10-467-962B-100	Sequence 100, App
c	10	24.4	26.2	3893	1	US-10-821-234-255	Sequence 255, App
	11	24.2	26.0	963	1	US-10-821-234-775	Sequence 775, App
	12	24	25.8	2748	1	US-10-526-731-4	Sequence 4, Appli
	13	23.8	25.6	1150	1	US-10-131-826A-531	Sequence 531, App
	14	23.8	25.6	5690	1	US-10-485-517-4	Sequence 4, Appli
c	15	23.8	25.6	14770	1	US-10-821-234-268	Sequence 268, App
	16	23.4	25.2	477	1	US-10-467-962B-82	Sequence 82, Appl
c	17	23.4	25.2	7008	1	US-10-821-234-758	Sequence 758, App
c	18	23	24.7	445	1	US-10-802-796-374	Sequence 374, App
	19	23	24.7	1152	7	US-11-074-176-77	Sequence 77, Appl
c	20	23	24.7	1849	7	US-11-015-546A-19	Sequence 19, Appl
c	21	23	24.7	1956	1	US-10-994-820A-33	Sequence 33, Appl
c	22	23	24.7	2292	7	US-11-013-247A-34	Sequence 34, Appl
	23	22.8	24.5	585	1	US-10-793-626-621	Sequence 621, App
	24	22.8	24.5	1209	7	US-11-074-176-353	Sequence 353, App
	25	22.8	24.5	1224	7	US-11-074-176-185	Sequence 185, App
c	26	22.8	24.5	1675	9	US-11-082-389-35	Sequence 35, Appl
c	27	22.8	24.5	1758	9	US-11-082-389-33	Sequence 33, Appl
c	28	22.8	24.5	3769	1	US-10-793-626-4106	Sequence 4106, Ap
c	29	22.8	24.5	4249	1	US-10-793-626-4133	Sequence 4133, Ap
	30	22.4	24.1	1688	7	US-11-065-943-19	Sequence 19, Appl
	31	22.4	24.1	1688	7	US-11-065-943-21	Sequence 21, Appl
	32	22.4	24.1	1688	7	US-11-065-943-23	Sequence 23, Appl
	33	22.4	24.1	1688	7	US-11-065-943-25	Sequence 25, Appl
	34	22.4	24.1	1688	7	US-11-065-943-27	Sequence 27, Appl
	35	22.4	24.1	1688	7	US-11-065-943-29	Sequence 29, Appl
	36	22.4	24.1	1688	7	US-11-065-943-31	Sequence 31, Appl
	37	22.4	24.1	1688	7	US-11-065-943-33	Sequence 33, Appl
	38	22.4	24.1	1688	7	US-11-065-943-35	Sequence 35, Appl
	39	22.4	24.1	1688	7	US-11-065-943-37	Sequence 37, Appl
c	40	22.4	24.1	8424	1	US-10-821-234-47	Sequence 47, Appl
	41	22.2	23.9	45	1	US-10-839-799-110	Sequence 110, App
	42	22.2	23.9	84	1	US-10-839-799-100	Sequence 100, App
c	43	22.2	23.9	84	1	US-10-839-799-101	Sequence 101, App
	44	22.2	23.9	822	1	US-10-839-799-108	Sequence 108, App
c	45	22.2	23.9	1506	1	US-10-971-560-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-927-641-116/c
; Sequence 116, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/927,641
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 947
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-927-641-116

Query Match 30.3%; Score 28.2; DB 1; Length 947;
Best Local Similarity 56.1%; Pred. No. 1.7;
Matches 23; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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Qy          2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGU 42
              | |:  || |    ||:||:||:||:||:||:||:||:||:
Db        537 CAGTGCCCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 497
```

```
RESULT 2
US-10-509-422-1/c
; Sequence 1, Application US/10509422
; Publication No. US20050244825A1
; GENERAL INFORMATION:
;  APPLICANT: Liou, Simon
;  TITLE OF INVENTION: Human BMP2 Inducible Kinases
;  FILE REFERENCE: 004974.01015
;  CURRENT APPLICATION NUMBER: US/10/509,422
;  CURRENT FILING DATE:  2004-09-24
;  PRIOR APPLICATION NUMBER: PCT/EP03/080825
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/367,512
;  PRIOR FILING DATE: 2002-03-27
;  PRIOR APPLICATION NUMBER: US 60/406,936
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3507
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-509-422-1

  Query Match             30.3%;  Score 28.2;  DB 1;  Length 3507;
  Best Local Similarity   60.6%;  Pred. No. 2.1;
  Matches   20;  Conservative   10;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 GAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGU 42
               ||| : ||:||:||:||:||:||:||:||:| :
Db        1489 GAAGTAGGTGGTGGTGGTGGTGGTGGTGGTGCT 1457


RESULT 3
US-10-509-422-3/c
; Sequence 3, Application US/10509422
; Publication No. US20050244825A1
; GENERAL INFORMATION:
;  APPLICANT: Liou, Simon
;  TITLE OF INVENTION: Human BMP2 Inducible Kinases
;  FILE REFERENCE: 004974.01015
;  CURRENT APPLICATION NUMBER: US/10/509,422
;  CURRENT FILING DATE:  2004-09-24
;  PRIOR APPLICATION NUMBER: PCT/EP03/080825
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/367,512
;  PRIOR FILING DATE: 2002-03-27
;  PRIOR APPLICATION NUMBER: US 60/406,936
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3704
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-509-422-3

  Query Match             30.3%;  Score 28.2;  DB 1;  Length 3704;
  Best Local Similarity   60.6%;  Pred. No. 2.2;
  Matches   20;  Conservative   10;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 GAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGU 42
               ||| : ||:||:||:||:||:||:||:||:| :
Db        1589 GAAGTAGGTGGTGGTGGTGGTGGTGGTGGTGCT 1557


RESULT 4
US-10-821-234-839
; Sequence 839, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 839
;   LENGTH: 6497
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-839

  Query Match             30.1%;  Score 28;  DB 1;  Length 6497;
  Best Local Similarity   43.3%;  Pred. No. 2.8;
  Matches   26;  Conservative   14;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          16 GGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGU 75
               | :||:||:||:||:||:| :||:| :  ||||:       |  |:| :||     :|| :
Db        3179 GATGGTGGTGGTGGTGGTGATGGTGATGGGAACTGTTACCATGGTGATGATGCAATGCAT 3238


RESULT 5
US-10-131-826A-35/c
; Sequence 35, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C128
;  CURRENT APPLICATION NUMBER: US/10/131,826A
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
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;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 35
;   LENGTH: 3371
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-131-826A-35

  Query Match             28.4%;  Score 26.4;  DB 1;  Length 3371;
  Best Local Similarity   46.7%;  Pred. No. 7.6;
  Matches   28;  Conservative   11;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         15 CGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCG 74
              | |:||  |:||:||:||  |:|| ||:  |   : |    | | :| :| |:|||:| |
Db        508 CAGTGGGCGTGGTGGTGGCAGTGGCGGTGGGGTGTGCCACCACCATGGTGGATGGCTGGG 449


RESULT 6
US-10-793-626-4301/c
; Sequence 4301, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4301
;   LENGTH: 2536
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4301

  Query Match             27.1%;  Score 25.2;  DB 1;  Length 2536;
  Best Local Similarity   43.5%;  Pred. No. 17;
  Matches   27;  Conservative   12;  Mismatches   23;  Indels    0;  Gaps    0;

Qy         20 GUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAA 79
              | ||:| :|    :||:  :||: :  ||:||| | || |  : | |:| |:|  :|  |
Db       1718 GGGGTGATGCCTATGGTTTTGGTTTCTACTCCAAGAAAGGAATAGCATGACTGATTATGA 1659

Qy         80 AA 81
              ||
Db       1658 AA 1657


RESULT 7
US-10-821-234-766/c
; Sequence 766, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 766
;   LENGTH: 1065
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-766

  Query Match             26.9%;  Score 25;  DB 1;  Length 1065;
  Best Local Similarity   40.0%;  Pred. No. 16;
  Matches   26;  Conservative   14;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          4 GUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUU 63
              |:::||      ||:||:||:|| | :|   |:||  |:|     :|| :||   |:| :
Db        264 GTTTCCATGGCTGGTGGTGGTGGGGTTGTGAGTGGCAGTCGTGGGTCCGTGGCTGGTGGT 205

Qy         64 GAAUG 68
              |  :|
Db        204 GCCTG 200


RESULT 8
US-10-821-234-119/c
; Sequence 119, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 119
;   LENGTH: 2218
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-119

  Query Match             26.5%;  Score 24.6;  DB 1;  Length 2218;
  Best Local Similarity   47.3%;  Pred. No. 25;
  Matches   26;  Conservative   10;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         16 GGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGC 70
              ||:||:||:||:||:||:||: | |     |  |:|  : |  |  | :| |  ||
Db       1756 GGTGGTGGTGGTGGTGGTGGTTGAGACAGGGTCTCTGTTGCCCAGGCTGGAGTGC 1702


RESULT 9
US-10-467-962B-100/c
; Sequence 100, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
;  APPLICANT: Plesch, Gunnar
;  APPLICANT:  Blau, Astrid
;  APPLICANT:  Daeschner, Klaus
;  APPLICANT:  Klein, Mathieu
;  TITLE OF INVENTION: Identification of Herbicidally Active Substances
;  FILE REFERENCE: 2000_857
;  CURRENT APPLICATION NUMBER: US/10/467,962B
;  CURRENT FILING DATE:  2003-08-14
;  PRIOR APPLICATION NUMBER: PCT/EP02/01466
;  PRIOR FILING DATE: 2002-02-13
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 100
;   LENGTH: 2043
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2043)
;   OTHER INFORMATION: ORF K5J14.11, Linie 229091
```

US-10-467-962B-100

Query Match 26.2%; Score 24.4; DB 1; Length 2043;
Best Local Similarity 69.2%; Pred. No. 29;
Matches 18; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

```
Qy         12 AAUCGGUGGUGGUGGUGGUGGUGGUG 37
              || |||:||:||:||:||:||:||:|
Db         89 AAGCGGTGGTGGTGGTGGTGGTGGTG 64
```

RESULT 10
US-10-821-234-255/c
; Sequence 255, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 255
; LENGTH: 3893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-255

Query Match 26.2%; Score 24.4; DB 1; Length 3893;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 16; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

```
Qy         17 GUGGUGGUGGUGGUGGUGGUGGUGGU 42
              |:||:||:||:||:||:||: |:||:
Db       2641 GTGGTGGTGGTGGTGGTGGTCGTGGT 2616
```

RESULT 11
US-10-821-234-775
; Sequence 775, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 775
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-775

Query Match 26.0%; Score 24.2; DB 1; Length 963;
Best Local Similarity 51.4%; Pred. No. 29;
Matches 19; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

```
Qy          3 UGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGU 39
              :| ::| | || |  :||:||:||: |:|| ||:||:
Db        591 TGGTTCTGGAAACTTTGGTGGTGGTCGTGGAGGTGGT 627
```

RESULT 12
US-10-526-731-4
; Sequence 4, Application US/10526731
; Publication No. US20050244437A1
; GENERAL INFORMATION:
; APPLICANT: AKZO Nobel N.V.
; TITLE OF INVENTION: live attenuated parasite vaccine
; FILE REFERENCE: 2002-017-EP
; CURRENT APPLICATION NUMBER: US/10/526,731
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: EP 02078953
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Toxoplasma gondii
US-10-526-731-4

Query Match 25.8%; Score 24; DB 1; Length 2748;
Best Local Similarity 54.2%; Pred. No. 40;
Matches 26; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

```
Qy         38 GUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGC 85
              |:||:|:|  | |||:|| ||  |  |||: | :|||  | || |: |
Db       2021 GTGGTCTGTGCGCCATGGCACAGGCAGAATCGTTGCGGTACAAGCTTC 2068
```

RESULT 13
US-10-131-826A-531
; Sequence 531, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-531

Query Match 25.6%; Score 23.8; DB 1; Length 1150;
Best Local Similarity 51.2%; Pred. No. 39;
Matches 22; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

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Qy         16 GGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAAC 58
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Db        841 GGTGGGGGTGGTGGTGGGGGTAGTGGCCTTTGCTGTGTGCCAC 883
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RESULT 14
US-10-485-517-4
; Sequence 4, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 5690
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-485-517-4

Query Match 25.6%; Score 23.8; DB 1; Length 5690;
Best Local Similarity 35.8%; Pred. No. 53;
Matches 24; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

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              | :|:::|||       :||:  :  :||:|  ||:|| | :     | | |: | | |:
Db        520 GGTGTTTCCGGCTCGCTTGGTACTTCTGGTGTCGGTGGCGTTGGTGGCACGATTGGAGGT 579

Qy         61 GUUGAAU 67
              |::| |:
Db        580 GTTGTAT 586
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RESULT 15
US-10-821-234-268/c
; Sequence 268, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 268
; LENGTH: 14770
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-268

Query Match 25.6%; Score 23.8; DB 1; Length 14770;
Best Local Similarity 59.3%; Pred. No. 64;
Matches 16; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

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Qy         16 GGUGGUGGUGGUGGUGGUGGUGGUGGU 42
              ||:||:||:||: |:||:||: |:||:
Db      12126 GGTGGTGGTGGTAGTGGTGGTAGTGGT 12100
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Search completed: November 24, 2005, 04:56:48
Job time : 195 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:17:24 ; Search time 186 Seconds
(without alignments)
37.796 Million cell updates/sec

Title: SEQ-NEW
Perfect score: 83
Sequence: 1 avseiqlmhnlggggg 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	71	85.5	450	3	AAY96988	Aay96988 Human tet
2	69	83.1	31	3	AAY96975	Aay96975 Parathyro
3	62	74.7	31	3	AAY96973	Aay96973 Parathyro
4	62	74.7	38	2	AAR58104	Aar58104 [Gly13]-h
5	59	71.1	12	9	ADZ76826	Adz76826 Parathyro
6	59	71.1	13	6	ABG76365	Abg76365 Mutant pe
7	59	71.1	14	3	AAB01861	Aab01861 [Ala1]-pa
8	59	71.1	14	4	AAB96896	Aab96896 Rat parat
9	59	71.1	14	4	AAB84776	Aab84776 Native ra
10	59	71.1	14	8	ADR14864	Adr14864 Amino aci
11	59	71.1	14	8	ADU24382	Adu24382 Novel hum
12	59	71.1	14	9	ADW88336	Adw88336 Rat parat
13	59	71.1	15	9	ADZ76832	Adz76832 Parathyro
14	59	71.1	21	6	ABP71487	Abp71487 Rat parat
15	59	71.1	21	9	ADW88343	Adw88343 Rat parat
16	59	71.1	27	3	AAY98016	Aay98016 Human ami
17	59	71.1	27	3	AAY98049	Aay98049 Human par
18	59	71.1	27	3	AAY98045	Aay98045 Human par
19	59	71.1	28	3	AAY98048	Aay98048 Human par
20	59	71.1	28	3	AAY98044	Aay98044 Human par
21	59	71.1	30	5	AAU73060	Aau73060 Parathyro
22	59	71.1	30	8	ADQ75375	Adq75375 PTH/PTHrP
23	59	71.1	31	2	AAY04203	Aay04203 Human par
24	59	71.1	31	3	AAY96978	Aay96978 PTH-rP fu
25	59	71.1	31	7	ADI24779	Adi24779 Parathyro
26	59	71.1	33	3	AAY98015	Aay98015 Human ami
27	59	71.1	34	1	AAP82177	Aap82177 Sequence
28	59	71.1	34	2	AAR07920	Aar07920 Rat parat
29	59	71.1	34	2	AAR07917	Aar07917 Rat parat
30	59	71.1	34	2	AAR62432	Aar62432 Accelerat
31	59	71.1	34	2	AAR99980	Aar99980 Rat parat
32	59	71.1	34	2	AAW19996	Aaw19996 Cyclised
33	59	71.1	34	2	AAW20002	Aaw20002 Cyclised
34	59	71.1	34	2	AAW20008	Aaw20008 Cyclised
35	59	71.1	34	3	AAY98014	Aay98014 Human ami
36	59	71.1	34	4	AAB91100	Aab91100 Parathyro
37	59	71.1	34	4	AAB96897	Aab96897 Rat parat
38	59	71.1	34	4	AAB84777	Aab84777 Native hu
39	59	71.1	34	5	AAU73037	Aau73037 Parathyro
40	59	71.1	34	6	ABP71499	Abp71499 Rat parat
41	59	71.1	34	6	AAO27426	Aao27426 Mouse mat
42	59	71.1	34	6	AAO27425	Aao27425 Rat matur
43	59	71.1	34	8	ADP04395	Adp04395 Norway ra
44	59	71.1	34	8	ADQ75352	Adq75352 PTH/PTHrP
45	59	71.1	34	8	ADR14832	Adr14832 Amino aci
46	59	71.1	34	8	ADT94476	Adt94476 Exemplary
47	59	71.1	34	9	ADX15519	Adx15519 Rat PTH (
48	59	71.1	35	2	AAR74466	Aar74466 Parathyro
49	59	71.1	36	2	AAR58248	Aar58248 N-Dimethy
50	59	71.1	36	2	AAR58026	Aar58026 N-alpha-m
51	59	71.1	36	2	AAR58262	Aar58262 [Ala1]-hP
52	59	71.1	37	4	AAB86231	Aab86231 Rat parat
53	59	71.1	38	2	AAR58019	Aar58019 N-alpha-m
54	59	71.1	84	5	AAE18393	Aae18393 Rat PTH p
55	59	71.1	84	5	AAE23747	Aae23747 Rat PTH p
56	59	71.1	84	5	AAU73023	Aau73023 Parathyro
57	59	71.1	84	6	ABG72602	Abg72602 Rat bioac
58	59	71.1	84	6	ABG72603	Abg72603 Mouse bio
59	59	71.1	84	7	ADA39531	Ada39531 Rat parat
60	59	71.1	84	8	ADF77381	Adf77381 Parathyro
61	59	71.1	84	8	ADQ75338	Adq75338 PTH/PTHrP
62	59	71.1	84	8	ADT98118	Adt98118 Mouse par
63	59	71.1	84	8	ADT98117	Adt98117 Rat parat
64	59	71.1	84	9	ADX15518	Adx15518 Rat PTH (
65	59	71.1	84	9	ADX15531	Adx15531 Rat PTH (
66	59	71.1	84	9	ADZ76842	Adz76842 Rat parat
67	59	71.1	84	9	ADZ76843	Adz76843 Mouse par
68	59	71.1	84	9	ADZ76835	Adz76835 Rat parat
69	59	71.1	84	9	ADZ76836	Adz76836 Mouse par
70	59	71.1	115	1	AAP80308	Aap80308 Sequence
71	59	71.1	115	7	ADD47895	Add47895 Rat Prote
72	59	71.1	115	8	ADJ36448	Adj36448 Mus muscu
73	59	71.1	115	8	ADJ36460	Adj36460 Mus muscu
74	59	71.1	115	8	ADJ36472	Adj36472 Rat parat
75	59	71.1	115	8	ADJ36455	Adj36455 Rat parat
76	59	71.1	115	8	ADJ36470	Adj36470 Rat parat
77	58	69.9	38	2	AAR58024	Aar58024 [Ala1,Ile
78	57	68.7	31	2	AAY04204	Aay04204 Human par
79	57	68.7	31	7	ADI24780	Adi24780 Parathyro
80	57	68.7	35	2	AAR74470	Aar74470 Parathyro
81	56	67.5	12	9	ADZ76824	Adz76824 Parathyro
82	56	67.5	13	2	AAW99450	Aaw99450 Human par
83	56	67.5	13	6	ABG76366	Abg76366 Mutant pe
84	56	67.5	14	3	AAB01859	Aab01859 Human par
85	56	67.5	14	4	AAB96894	Aab96894 Human par
86	56	67.5	14	4	AAB84773	Aab84773 Native hu
87	56	67.5	14	8	ADR14863	Adr14863 Amino aci
88	56	67.5	14	8	ADU24391	Adu24391 Human par
89	56	67.5	15	9	ADZ76830	Adz76830 Parathyro
90	56	67.5	17	2	AAR94192	Aar94192 Human par
91	56	67.5	21	6	ABP71486	Abp71486 Human par
92	56	67.5	21	9	ADW88342	Adw88342 Human par
93	56	67.5	27	3	AAY98019	Aay98019 Human ami
94	56	67.5	27	3	AAY98047	Aay98047 Human par
95	56	67.5	27	3	AAY98053	Aay98053 Human par
96	56	67.5	28	2	AAR88838	Aar88838 Human par
97	56	67.5	28	2	AAR88837	Aar88837 Human par

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    98       56   67.5      28  3  AAY98046                  Aay98046 Human par
    99       56   67.5      28  3  AAY98052                  Aay98052 Human par
   100       56   67.5      28  4  AAB81074                  Aab81074 Human par

                                ALIGNMENTS

RESULT 1
AAY96988
ID   AAY96988 standard; protein; 450 AA.
XX
AC   AAY96988;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Human tethered PTH-1 receptor, Tether-R11.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_sequence
FT                   /note= "Human PTH-1 receptor residues 1-23"
FT   Peptide         24. .34
FT                   /label= PTH(1-11)
FT   Peptide         35. .38
FT                   /label= Linker
FT   Protein         39. .450
FT                   /label= PTH-1_receptor
FT                   /note= "Human PTH-1 receptor residues 182-593"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   N-PSDB; AAA51737.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Example 4; Fig 19; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 450 AA;

  Query Match             85.5%;  Score 71;  DB 3;  Length 450;
  Best Local Similarity   93.3%;  Pred. No. 0.0085;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGGG 15
              ||||||||||  ||||
Db         24 AVSEIQLMHNRGGGG 38


RESULT 2
AAY96975
ID   AAY96975 standard; peptide; 31 AA.
XX
AC   AAY96975;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Parathyroid hormone functional domain conjugate peptide PG7.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .9
FT                   /label= PTH_N-terminal_signaling_domain
FT                   /note= "residues 1-9"
FT   Peptide         10. .16
FT                   /label= linker
FT   Peptide         17. .31
FT                   /label= PTH_C-terminal_binding_portion
FT                   /note= "residues 17-31"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   N-PSDB; AAA51730.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 7; Page 93; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
```

```
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 31 AA;

  Query Match             83.1%;  Score 69;  DB 3;  Length 31;
  Best Local Similarity   87.5%;  Pred. No. 0.00085;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGGGG 16
              |||||||||  |||||
Db          1 AVSEIQLMHGGGGGGG 16


RESULT 3
AAY96973
ID   AAY96973 standard; peptide; 31 AA.
XX
AC   AAY96973;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Parathyroid hormone functional domain conjugate peptide PG5.
XX
KW   PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW   resorption; remodeling; tether1; osteoporosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .9
FT                   /label= PTH_N-terminal_signaling_domain
FT                   /note= "residues 1-9"
FT   Peptide         10. .14
FT                   /label= linker
FT   Peptide         15. .30
FT                   /label= PTH_C-terminal_binding_portion
FT                   /note= "residues 15-31"
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
DR   N-PSDB; AAA51729.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 7; Page 92-93; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 31 AA;

  Query Match             74.7%;  Score 62;  DB 3;  Length 31;
  Best Local Similarity   87.5%;  Pred. No. 0.011;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 AVSEIQLMHNLGGGGG 16
              |||||||||  |||||
Db          1 AVSEIQLMH--GGGGG 14


RESULT 4
AAR58104
ID   AAR58104 standard; peptide; 38 AA.
XX
AC   AAR58104;
XX
DT   20-SEP-1994  (first entry)
XX
DE   [Gly13]-hPTH(1-38)-OH.
XX
KW   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion;
KW   fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
XX
OS   Synthetic.
XX
PN   GB2269176-A.
XX
PD   02-FEB-1994.
XX
PF   12-JUL-1993;   93GB-00014384.
XX
PR   15-JUL-1992;   92GB-00015009.
PR   18-DEC-1992;   92GB-00026415.
PR   23-DEC-1992;   92GB-00026859.
PR   23-DEC-1992;   92GB-00026861.
PR   28-JAN-1993;   93GB-00001691.
PR   28-JAN-1993;   93GB-00001692.
PR   14-APR-1993;   93GB-00007673.
PR   19-APR-1993;   93GB-00008033.
XX
PA   (SANO ) SANDOZ LTD.
XX
PI   Lewis I,  Schneider H,  Waelchli R,  Rainer A;
XX
DR   WPI; 1994-018352/03.
XX
PT   New active para-thyroid hormone variants - used for treating or
PT   preventing osteoporosis etc.
XX
PS   Example 101; Page 39; 92pp; English.
XX
CC   This peptide is an example of a highly generic formula covering
CC   parathyroid hormone variants useful for treating or preventing bone
CC   conditions associated with calcium depletion/resorption, in cases where
CC   calcium fixation is required (esp. osteoporosis) or to treat
CC   hypoparathyroidism
XX
SQ   Sequence 38 AA;

  Query Match             74.7%;  Score 62;  DB 2;  Length 38;
  Best Local Similarity   92.3%;  Pred. No. 0.014;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 AVSEIQLMHNLGG 13
              :|||||||||||||
Db          1 SVSEIQLMHNLGG 13


RESULT 5
ADZ76826
ID   ADZ76826 standard; peptide; 12 AA.
XX
AC   ADZ76826;
XX
DT   14-JUL-2005  (first entry)
XX
DE   Parathyroid hormone (PTH) (1-12) antigenic peptide, SEQ ID NO: 5.
XX
KW   Parathormone; PTH; hormone; antigen.
XX
OS   Mus musculus.
OS   Rattus sp.
XX
PN   US2005095236-A1.
XX
PD   05-MAY-2005.
XX
PF   29-NOV-2004; 2004US-00998927.
XX
PR   05-DEC-2000; 2000US-00730174.
XX
PA   (ZAHR/) ZAHRADNIK R J.
PA   (LAVI/) LAVIGNE J R.
XX
PI   Zahradnik RJ,  Lavigne JR;
XX
DR   WPI; 2005-344980/35.
XX
PT   Producing antibodies to the N-terminal portion of (1-84) parathyroid
PT   hormone (PTH) by administering a first peptide antigen to a host animal,
PT   useful in determining bioactive intact PTH levels in serum, plasma and/or
PT   cell culture media.
XX
PS   Claim 1; SEQ ID NO 5; 13pp; English.
XX
CC   The present invention relates to a method of producing an antibody to the
CC   N-terminal portion of (1-84) parathyroid hormone (PTH) which comprises
CC   administering N-terminal peptide antigens corresponding to amino acid
CC   residues 2-12, 1-12, 2-15 and 1-15 of PTH. The methods and compositions
CC   of the invention are useful in determining bioactive intact PTH levels in
CC   serum, plasma and/or cell culture media and antibodies possessing a high
CC   degree of species cross-reactivity. The present sequence is a parathyroid
CC   hormone (PTH) (1-12) antigenic N-terminal peptide. This N-terminal
CC   peptide sequence is obtained from mouse and rat species.
XX
SQ   Sequence 12 AA;

  Query Match             71.1%;  Score 59;  DB 9;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 6
ABG76365
ID   ABG76365 standard; peptide; 13 AA.
XX
AC   ABG76365;
XX
DT   19-MAY-2003  (first entry)
XX
DE   Mutant peptide #2 derived from human parathyroid hormone (hPTH).
XX
KW   Human; three-dimensional epitope; human parathyroid hormone; hPTH;
KW   bioactive hPTH; antibody production; hyperparathyroidism; antithyroid;
KW   hypoparathyroidism; immunostimulant; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003003986-A2.
XX
PD   16-JAN-2003.
XX
PF   03-JUL-2002; 2002WO-US021356.
XX
PR   03-JUL-2001; 2001US-00898398.
XX
PA   (QUES-) QUEST DIAGNOSTICS INVESTMENTS INC.
XX
PI   Hutchison JS;
XX
DR   WPI; 2003-229379/22.
XX
PT   Producing antibodies to a three-dimensional epitope of a bioactive human
PT   parathyroid hormone for diagnosing or treating e.g., hyperparathyroidism
PT   by immunizing an animal with the hormone and recovering the antibodies.
XX
PS   Disclosure; Page 10; 69pp; English.
XX
CC   The present invention relates to a method for producing antibodies to a
CC   three-dimensional epitope of bioactive human parathyroid hormone (hPTH).
CC   The method comprises immunising an animal with the bioactive hPTH and
CC   recovering antibodies from the animal. The antibodies specifically
CC   recognise the three-dimensional structure of the bioactive hPTH. The
CC   method is useful for manufacturing a medicament for diagnosing or
CC   treating hyperparathyroidism or hypoparathyroidism. ABG76364-ABG76370
CC   represent mutants or "variants" of peptide sequences from hPTH
XX
SQ   Sequence 13 AA;

  Query Match             71.1%;  Score 59;  DB 6;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 7
AAB01861
ID   AAB01861 standard; peptide; 14 AA.
XX
AC   AAB01861;
XX
DT   11-SEP-2000  (first entry)
XX
DE   [Ala1]-parathyroid hormone peptide(1-14), SEQ ID NO:5.
XX
KW   Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KW   calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KW   bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   14
FT                   /note= "C-terminal amide"
XX
PN   WO200023594-A1.
XX
PD   27-APR-2000.
XX
PF   20-OCT-1999;   99WO-US024481.
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XX
PR   22-OCT-1998;   98US-0105530P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-339693/29.
XX
PT   Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT   acids that encode them, useful for treating osteoporosis.
XX
PS   Claim 3; Page 47; 73pp; English.
XX
CC   The invention relates to a novel parathyroid hormone (PTH) peptide
CC   (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC   biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC   B01869). The peptides of the invention are at least 85% identical to the
CC   generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC   Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC   Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC   provided that the peptide is not PTHrP(1-14). The peptides of the
CC   invention also encompass fragments of peptides of the invention
CC   consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC   terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC   and is necessary for the normal function of the gastrointestinal,
CC   skeletal, neurological system, neuromuscular and cardiovascular systems.
CC   It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC   and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC   effect on the skeleton, and mediates calcium reabsorption, enhances
CC   phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC   calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC   the renal and skeletal actions of PTH, and also bind to the PTH-1
CC   receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC   invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC   AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC   B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC   conditions characterised by a decrease in bone mass, such as
CC   osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC   medical disorders that arise from excessive or altered action of the PTH-
CC   1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC   useful in the determination of rates of bone formation, bone resorption
CC   and/or bone remodelling in a patient. The peptides of the invention are
CC   "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC   conventional synthetic chemistry, and can be delivered to a patient via
CC   non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC   PTH-1/PTH-2 receptor agonists
XX
SQ   Sequence 14 AA;

  Query Match             71.1%;  Score 59;  DB 3;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 8
AAB96896
ID   AAB96896 standard; peptide; 14 AA.
XX
AC   AAB96896;
XX
DT   13-JUL-2001  (first entry)
XX
DE   Rat parathyroid hormone(1-14).
XX
KW   Rat; human; parathyroid hormone derivative; calcium homeostasis;
KW   hypercalcaemia; anaemia; bone disease; renal impairment; ulcer; myopathy;
KW   neuropathy; hyperparathyroidism; osteoporosis; fracture;
KW   cartilage disorder.
XX
OS   Rattus sp.
XX
PN   WO200123427-A1.
XX
PD   05-APR-2001.
XX
PF   25-FEB-2000; 2000WO-US004716.
XX
PR   29-SEP-1999;   99US-0156927P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2001-343161/36.
XX
PT   Novel amino acid encoding polypeptides useful in the treatment of
PT   osteoporosis.
XX
PS   Example 2; Page 64; 100pp; English.
XX
CC   The present invention provides a number of parathyroid hormone
CC   derivatives based on the rat and human hormone sequences. These peptides
CC   can be used in the treatment of human skeletal conditions, including
CC   osteoporosis, fractures and cartilage disorders, disruption of calcium
CC   homeostasis, which may cause severe bone disease, anaemia, renal
CC   impairment, ulcers, myopathy and neuropathy, hypercalcaemia and
CC   hyperparathyroidism. The present peptide was used in the exemplification
CC   of the invention
XX
SQ   Sequence 14 AA;

  Query Match             71.1%;  Score 59;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 9
AAB84776
ID   AAB84776 standard; peptide; 14 AA.
XX
AC   AAB84776;
XX
DT   25-JUL-2001  (first entry)
XX
DE   Native rat parathyroid hormone peptide fragment #1.
XX
KW   Osteopathic; calcium homeostasis regulator; parathyroid hormome; PTH;
KW   bone mass; osteoporosis.
XX
OS   Rattus sp.
XX
PN   WO200123521-A2.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-US026818.
XX
PR   29-SEP-1999;   99US-0156927P.
PR   25-FEB-2000; 2000US-0185060P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Juppner H;
XX
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```
DR   WPI; 2001-374252/39.
XX
PT   New Parathyroid hormone (PTH) derivatives useful for treating conditions
PT   characterized by decreases in bone mass.
XX
PS   Example 2; Page 67; 97pp; English.
XX
CC   The present invention relates to parathyroid hormome (PTH) polypeptide
CC   derivatives, and the present sequence is one such derivative. PTH is a
CC   major regulator of calcium homeostasis. The PTH polypeptide derivatives
CC   are useful for treating conditions characterised by decreases in bone
CC   mass, such as old age osteoporosis and post-menopausal osteoporosis. The
CC   polypeptides are also useful for determining rates of bone reformation,
CC   bone resorption and/or bone remodeling, by administering the polypeptide
CC   to the patient and determining the uptake of the peptide into the bone,
CC   and effective bone mass-increasing amount to the peptide is administered
CC   by providing to the patient DNA encoding the peptide and expressing the
CC   peptide in vivo. The levels of cAMP and inositol phosphate can also be
CC   increased in a mammalian cell having PTH-1 receptors, by contacting the
CC   cell with a sufficient amount of the polypeptide
XX
SQ   Sequence 14 AA;

  Query Match             71.1%;  Score 59;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 10
ADR14864
ID   ADR14864 standard; peptide; 14 AA.
XX
AC   ADR14864;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Amino acid sequence of a parathyroid hormone fragment.
XX
KW   bone mass; parathyroid hormone; PTH; lactam bridge; agonist;
KW   PTH-1 receptor; old age; post-menopausal osteoporosis; osteoporosis.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   14
FT                   /note= "amidated residue"
XX
PN   WO2004067021-A1.
XX
PD   12-AUG-2004.
XX
PF   24-JAN-2003; 2003WO-US002155.
XX
PR   24-JAN-2003; 2003WO-US002155.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT;
XX
DR   WPI; 2004-580854/56.
XX
PT   Treating mammalian conditions characterized by a decrease in bone mass
PT   e.g. old age or post-menopausal osteoporosis by administering to a
PT   subject a biologically active peptide or its analogs, fragments, salts or
PT   N- or C- derivatives.
XX
PS   Disclosure; SEQ ID NO 37; 63pp; English.
XX
CC   The specification describes a method for treating mammalian conditions
CC   characterized by a decrease in bone mass. The method comprises
CC   administering to a subject a biologically active peptide of a formula
CC   given in the specification. The peptide is a parathyroid hormone (PTH)
CC   derivative containing amino acid substitutions at selected positions in
CC   the polypeptide as well as derivatives containing lactam bridges between
CC   residues 6 and 10. The derivatives function as agonists of the PTH-1
CC   receptor. The method is useful in treating mammalian conditions
CC   characterized by a decrease in bone mass e.g. old age or post-menopausal
CC   osteoporosis. The present sequence represents a native rat PTH fragment.
XX
SQ   Sequence 14 AA;

  Query Match             71.1%;  Score 59;  DB 8;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 11
ADU24382
ID   ADU24382 standard; peptide; 14 AA.
XX
AC   ADU24382;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Novel human parathyroid hormone-derived active peptide SeqID17.
XX
KW   biologically active peptide; parathyroid hormone analogue; endocrine-Gen;
KW   antithyroid; cardiovascular-Gen; CNS-Gen; gastrointestinal-Gen;
KW   osteopathic; cAMP agonist; bone calcification promoter;
KW   parathyroid hormone-1 receptor agonist; calcium antagonist; bone mass;
KW   bone reformation; bone resorption; bone remodeling; osteoporosis;
KW   osteopenia; bone fracture; cartilage disorder; OTH-1 receptor; human.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   14
FT                   /note= "C-terminal amide"
XX
PN   WO2004093902-A1.
XX
PD   04-NOV-2004.
XX
PF   19-MAR-2003; 2003WO-US008261.
XX
PR   19-MAR-2003; 2003WO-US008261.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Gardella TJ,  Potts JT,  Kronenberg HM,  Shimizu N,  Carter P;
XX
DR   WPI; 2004-795421/78.
XX
PT   New conformationally constrained parathyroid hormone analogs and
PT   derivatives of those homologs, useful for raising cAMP levels in cells
PT   and treating conditions such as hyperparathyroidism and hypercalcemia.
XX
PS   Disclosure; SEQ ID NO 17; 88pp; English.
XX
CC   This invention relates to a novel biologically active peptide
CC   (conformationally constrained parathyroid hormone analogues and
CC   derivatives of those homologues). The invention may be useful for the
CC   development of compounds with an endocrine-Gen, antithyroid,
CC   cardiovascular-Gen, CNS-Gen, gastrointestinal-Gen or osteopathic activity
```

CC acting as a cAMP agonist, bone calcification promoter, agonist of
CC parathyroid hormone-1 receptor or calcium antagonist. The invention may
CC be useful for treating mammalian conditions associated with decrease in
CC bone mass or for determining rates of bone reformation, bone resorption
CC and/or bone remodeling. The invention may also be useful for prophylaxis
CC and/or treatment of disorders associated with undesired bone loss, for
CC example osteoporosis, osteopenia, fractures and cartilage disorders, and
CC for treating a medical disorder that results from altered or excessive
CC action of the OTH-1 receptor. The present sequence is that of a human
CC parathyroid hormone-derived biologically active peptide of the invention.
XX
SQ Sequence 14 AA;

Query Match 71.1%; Score 59; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
||||||||||||
Db 1 AVSEIQLMHNLG 12

RESULT 12
ADW88336
ID ADW88336 standard; peptide; 14 AA.
XX
AC ADW88336;
XX
DT 21-APR-2005 (first entry)
XX
DE Rat parathyroid hormone.
XX
KW Cardiovascular-gen.; CNS-gen.; gastrointestinal-gen.; endocrine-gen.;
KW antithyroid; parathormone; hypercalcemia; metabolic disorder.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Modified-site 14
FT /note= "C-terminal amide"
XX
PN WO2005009358-A2.
XX
PD 03-FEB-2005.
XX
PF 16-JUL-2004; 2004WO-US022830.
XX
PR 17-JUL-2003; 2003US-0487589P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Gardella TJ;
XX
DR WPI; 2005-132386/14.
XX
PT New conformationally constrained parathyroid hormone analogs useful in
PT the treatment of e.g. hypercalcemia primary and hyperparathyroidism.
XX
PS Disclosure; SEQ ID NO 26; 49pp; English.
XX
CC The invention provides novel antagonists of the juxtaposition (J) domain
CC of the parathyroid hormone (PTH or parathormone) receptor. These
CC antagonists contain amino acid substitutions at selected positions in
CC truncated PTH and PTH-related polypeptide and function by selectively
CC binding the J domain of the receptor. The J domain is the region of the
CC receptor (P1R) that spans the seven transmembrane domain and the
CC extracellular loops. P1R polypeptide antagonists of the invention can be
CC used to treat conditions relating to PH/P1R hyperactivity, such as
CC hypercalcemia including malignant hypercalcemia (claimed), primary
CC hyperparathyroidism, and Jansen's chondrodysplasia. They can also be used
CC to identify other ligands (e.g. using a high-throughput screen) that bind
CC to P1R, such as small molecule PTH mimetic compounds, or for the
CC pharmacological analysis of P1R ligands for their selectivity, e.g. for
CC the J domain. The present sequence is that of rat PTH(1-14). PTH
CC derivatives of the invention contain changes in sequence relative to this
CC wild-type sequence. Note: this sequence is given as SEQ ID NO:26 in
CC Figure 1 of the specification, but is different from the sequence given
CC in SEQ ID NO:26 on page 16 ADW88342.
XX
SQ Sequence 14 AA;

Query Match 71.1%; Score 59; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
||||||||||||
Db 1 AVSEIQLMHNLG 12

RESULT 13
ADZ76832
ID ADZ76832 standard; peptide; 15 AA.
XX
AC ADZ76832;
XX
DT 14-JUL-2005 (first entry)
XX
DE Parathyroid hormone (PTH) (1-15) antigenic peptide, SEQ ID NO: 11.
XX
KW Parathormone; PTH; hormone; antigen.
XX
OS Mus musculus.
OS Rattus sp.
XX
PN US2005095236-A1.
XX
PD 05-MAY-2005.
XX
PF 29-NOV-2004; 2004US-00998927.
XX
PR 05-DEC-2000; 2000US-00730174.
XX
PA (ZAHR/) ZAHRADNIK R J.
PA (LAVI/) LAVIGNE J R.
XX
PI Zahradnik RJ, Lavigne JR;
XX
DR WPI; 2005-344980/35.
XX
PT Producing antibodies to the N-terminal portion of (1-84) parathyroid
PT hormone (PTH) by administering a first peptide antigen to a host animal,
PT useful in determining bioactive intact PTH levels in serum, plasma and/or
PT cell culture media.
XX
PS Disclosure; SEQ ID NO 11; 13pp; English.
XX
CC The present invention relates to a method of producing an antibody to the
CC N-terminal portion of (1-84) parathyroid hormone (PTH) which comprises
CC administering N-terminal peptide antigens corresponding to amino acid
CC residues 2-12, 1-12, 2-15 and 1-15 of PTH. The methods and compositions
CC of the invention are useful in determining bioactive intact PTH levels in
CC serum, plasma and/or cell culture media and antibodies possessing a high
CC degree of species cross-reactivity. The present sequence is a parathyroid
CC hormone (PTH) (1-15) antigenic N-terminal peptide. This N-terminal
CC peptide sequence is obtained from mouse and rat species.
XX
SQ Sequence 15 AA;

Query Match 71.1%; Score 59; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
||||||||||||
Db 1 AVSEIQLMHNLG 12

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RESULT 14
ABP71487
ID   ABP71487 standard; peptide; 21 AA.
XX
AC   ABP71487;
XX
DT   15-MAY-2003  (first entry)
XX
DE   Rat parathyroid hormone (PTH) peptide fragment (residues 1-21).
XX
KW   PTH; parathyroid hormone; anabolic; cAMP; bone mass; osteopenia; rat.
XX
OS   Rattus sp.
XX
PN   WO2003009804-A2.
XX
PD   06-FEB-2003.
XX
PF   19-JUL-2002; 2002WO-US022922.
XX
PR   23-JUL-2001; 2001US-0306866P.
PR   02-OCT-2001; 2001US-0326212P.
XX
PA   (GARD/) GARDELLA T J.
XX
PI   Gardella TJ;
XX
DR   WPI; 2003-268010/26.
XX
PT   Conformationally constrained parathyroid hormone (PTH) analogs, useful
PT   for treating conditions characterized by decrease in bone mass (e.g.
PT   osteoporosis) or by the need for bone growth (e.g. in treating fractures
PT   or cartilage disorders).
XX
PS   Disclosure; Page 114; 135pp; English.
XX
CC   The invention relates to conformationally constrained parathyroid hormone
CC   (PTH) analogueues, in particular, derivatives of PTH (1-34), PTH (1-21),
CC   PTH (1-20), PTH (1-19), PTH (1-318), PTH (1-17), PTH (1-16), PTH (1-15),
CC   PTH (1-14), PTH (1-13), PTH (1-12), PTH (1-11), and PTH (1-10)
CC   polypeptides. The PTH peptide analogues are useful for treating mammalian
CC   conditions characterized by decrease in bone mass (e.g. old age
CC   osteoporosis, post-menopausal osteoporosis) or by the need for bone
CC   growth for e.g. in treating fractures or cartilage disorders and for
CC   raising cyclic adenosine monophosphate (cAMP) levels in cells. They are
CC   also useful for treating osteopenia. The PTH peptide analogues can also
CC   be used as diagnostic probes, as antigens to prepare antibodies for use
CC   as diagnostic probes and as molecular weight markers. The present
CC   sequence represents a rat native PTH peptide fragment
XX
SQ   Sequence 21 AA;

  Query Match             71.1%;  Score 59;  DB 6;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.022;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 15
ADW88343
ID   ADW88343 standard; peptide; 21 AA.
XX
AC   ADW88343;
XX
DT   21-APR-2005  (first entry)
XX
DE   Rat parathyroid hormone.
XX
KW   Cardiovascular-gen.; CNS-gen.; gastrointestinal-gen.; endocrine-gen.;
KW   antithyroid; parathormone; hypercalcemia; metabolic disorder.
XX
OS   Rattus sp.
XX
PN   WO2005009358-A2.
XX
PD   03-FEB-2005.
XX
PF   16-JUL-2004; 2004WO-US022830.
XX
PR   17-JUL-2003; 2003US-0487589P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Gardella TJ;
XX
DR   WPI; 2005-132386/14.
XX
PT   New conformationally constrained parathyroid hormone analogs useful in
PT   the treatment of e.g. hypercalcemia primary and hyperparathyroidism.
XX
PS   Disclosure; SEQ ID NO 27; 49pp; English.
XX
CC   The invention provides novel antagonists of the juxtaposition (J) domain
CC   of the parathyroid hormone (PTH or parathormone) receptor. These
CC   antagonists contain amino acid substitutions at selected positions in
CC   truncated PTH and PTH-related polypeptide and function by selectively
CC   binding the J domain of the receptor. The J domain is the region of the
CC   receptor (P1R) that spans the seven transmembrane domain and the
CC   extracellular loops. P1R polypeptide antagonists of the invention can be
CC   used to treat conditions relating to PH/P1R hyperactivity, such as
CC   hypercalcemia including malignant hypercalcemia (claimed), primary
CC   hyperparathyroidism, and Jansen's chondrodysplasia. They can also be used
CC   to identify other ligands (e.g. using a high-throughput screen) that bind
CC   to P1R, such as small molecule PTH mimetic compounds, or for the
CC   pharmacological analysis of P1R ligands for their selectivity, e.g. for
CC   the J domain. The present sequence is that of rat PTH(1-21). PTH
CC   derivatives of the invention contain changes in sequence relative to this
CC   wild-type sequence. Note: this sequence is given as SEQ ID NO:27 on page
CC   16 of the specification, but is different from the sequence given in SEQ
CC   ID NO:27 in Figure 1 ADW88337.
XX
SQ   Sequence 21 AA;

  Query Match             71.1%;  Score 59;  DB 9;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.022;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 16
AAY98016
ID   AAY98016 standard; peptide; 27 AA.
XX
AC   AAY98016;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Human amino-terminal modified parathyroid hormone analogue # 7.
XX
KW   Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;
KW   signal transduction; osteoporosis; amino-terminal modification;
KW   bone disease; parathyroid hormone receptor; osteopaenia;
KW   hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
```

```
FT                   /note= "Ala is desamino residue"
XX
PN   WO200031137-A1.
XX
PD   02-JUN-2000.
XX
PF   23-NOV-1999;   99WO-US027656.
XX
PR   25-NOV-1998;   98US-0110152P.
XX
PA   (BRIN/) BRINGHURST F R.
PA   (TAKA/) TAKASU H.
PA   (GARD/) GARDELLA T J.
XX
PI   Bringhurst FR,  Takasu H,  Gardella TJ;
XX
DR   WPI; 2000-400045/34.
XX
PT   New parathyroid hormone (PTH) analogs having one or more amino acid
PT   substitutions that confer PTH-1/PTH-2 receptor agonist properties, useful
PT   for treating old age osteoporosis and post-menopausal osteoporosis.
XX
PS   Disclosure; Page 64; 69pp; English.
XX
CC   Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC   cells, initiating signal transduction. It has been identified that the
CC   carboxyl terminal of PTH is important for PTH receptor binding, while the
CC   amino terminal is important for signal transduction. The present sequence
CC   is a human PTH peptide, with an amino-terminal modification which results
CC   in effective activation of the PTH-2 receptor and therefore downstream
CC   signalling. Aberrant PTH activity has been implicated in a number of
CC   disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC   hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC   and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC   myeloma and epidermoid cancers of the head, neck and oesophagus. This
CC   peptide would be suitable for prophylaxis and treatment of the above
CC   disorders. In addition, the present sequence would be suitable for
CC   fracture repair. The present sequence is modified to have a desamino
CC   residue at position 1
XX
SQ   Sequence 27 AA;

  Query Match             71.1%;  Score 59;  DB 3;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.029;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 17
AAY98049
ID   AAY98049 standard; peptide; 27 AA.
XX
AC   AAY98049;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Human parathyroid hormone peptide # 9.
XX
KW   Human; parathyroid hormone; signal transduction; osteoporosis;
KW   osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;
KW   breast cancer; lung cancer; prostate cancer; multiple myeloma;
KW   hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
KW   osteopathic; PTH.
XX
OS   Homo sapiens.
XX
PN   WO200031266-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US027863.
XX
PR   25-NOV-1998;   98US-0109938P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Bringhurst FR,  Takasu H,  Gardella TJ,  Potts JT;
XX
DR   WPI; 2000-400076/34.
XX
PT   Novel biologically active peptide comprising a parathyroid hormone
PT   peptide derivative, useful for treating osteoporosis.
XX
PS   Disclosure; Page 69; 75pp; English.
XX
CC   Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC   cells, initiating signal transduction. It has been identified that the
CC   carboxyl terminal of PTH is important for PTH receptor binding, while the
CC   amino terminal is important for signal transduction. Various PTH peptides
CC   were produces with amino- and carboxy terminal modifications which had
CC   varying PTH receptor activation properties and therefore downstream
CC   signalling. Aberrant PTH activity has been implicated in a number of
CC   disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC   hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC   and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC   myeloma and epidermoid cancers of the head, neck and oesophagus. The
CC   present sequence is a PTH peptide, with an Ala residue at position 1 and
CC   a Glu residue at position 19. The Ala residue improves downstream
CC   signalling via phospholipase C (PLC), whereas the Glu residue reduces PLC
CC   signalling and ligand binding. PTH peptides with an Arg residue at
CC   position 19 have improved PLC signalling and ligand binding and so may be
CC   used as a PTH receptor agonist for the treatment of the above mentioned
CC   disorders and fracture repair
XX
SQ   Sequence 27 AA;

  Query Match             71.1%;  Score 59;  DB 3;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.029;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 18
AAY98045
ID   AAY98045 standard; peptide; 27 AA.
XX
AC   AAY98045;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Human parathyroid hormone peptide # 5.
XX
KW   Human; parathyroid hormone; signal transduction; osteoporosis;
KW   osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;
KW   breast cancer; lung cancer; prostate cancer; multiple myeloma;
KW   hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
KW   osteopathic; PTH.
XX
OS   Homo sapiens.
XX
PN   WO200031266-A1.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US027863.
XX
PR   25-NOV-1998;   98US-0109938P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
```

PI Bringhurst FR, Takasu H, Gardella TJ, Potts JT;
XX
DR WPI; 2000-400076/34.
XX
PT Novel biologically active peptide comprising a parathyroid hormone
PT peptide derivative, useful for treating osteoporosis.
XX
PS Disclosure; Page 68; 75pp; English.
XX
CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC cells, initiating signal transduction. It has been identified that the
CC carboxyl terminal of PTH is important for PTH receptor binding, while the
CC amino terminal is important for signal transduction. Various PTH peptides
CC were produces with amino- and carboxy terminal modifications which had
CC varying PTH receptor activation properties and therefore downstream
CC signalling. Aberrant PTH activity has been implicated in a number of
CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC myeloma and epidermoid cancers of the head, neck and oesophagus. The
CC present sequence is a PTH peptide, with an Ala residue at position 1 and
CC an Arg residue at position 19. The Ala and Arg residues both improve
CC downstream signalling via phospholipase C (PLC) and ligand binding. The
CC present peptide may therefore be used as a PTH receptor agonist for the
CC treatment of the above mentioned disorders. In addition, the present
CC sequence would be suitable for fracture repair
XX
SQ Sequence 27 AA;

```
  Query Match             71.1%;  Score 59;  DB 3;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.029;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12
```

RESULT 19
AAY98048
ID AAY98048 standard; peptide; 28 AA.
XX
AC AAY98048;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human parathyroid hormone peptide # 8.
XX
KW Human; parathyroid hormone; signal transduction; osteoporosis;
KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;
KW breast cancer; lung cancer; prostate cancer; multiple myeloma;
KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
KW osteopathic; PTH.
XX
OS Homo sapiens.
XX
PN WO200031266-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US027863.
XX
PR 25-NOV-1998; 98US-0109938P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Bringhurst FR, Takasu H, Gardella TJ, Potts JT;
XX
DR WPI; 2000-400076/34.
XX
PT Novel biologically active peptide comprising a parathyroid hormone
PT peptide derivative, useful for treating osteoporosis.
XX
PS Claim 8; Page 69; 75pp; English.
XX
CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC cells, initiating signal transduction. It has been identified that the
CC carboxyl terminal of PTH is important for PTH receptor binding, while the
CC amino terminal is important for signal transduction. Various PTH peptides
CC were produces with amino- and carboxy terminal modifications which had
CC varying PTH receptor activation properties and therefore downstream
CC signalling. Aberrant PTH activity has been implicated in a number of
CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC myeloma and epidermoid cancers of the head, neck and oesophagus. The
CC present sequence is a PTH peptide, with an Ala residue at position 1 and
CC a Glu residue at position 19. The Ala residue improves downstream
CC signalling via phospholipase C (PLC), whereas the Glu residue reduces PLC
CC signalling and ligand binding. PTH peptides with a Arg residue at
CC position 19 have improved PLC signalling and ligand binding and so may be
CC used as a PTH receptor agonist for the treatment of the above mentioned
CC disorders and fracture repair
XX
SQ Sequence 28 AA;

```
  Query Match             71.1%;  Score 59;  DB 3;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12
```

RESULT 20
AAY98044
ID AAY98044 standard; peptide; 28 AA.
XX
AC AAY98044;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human parathyroid hormone peptide # 4.
XX
KW Human; parathyroid hormone; signal transduction; osteoporosis;
KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;
KW breast cancer; lung cancer; prostate cancer; multiple myeloma;
KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
KW osteopathic; PTH.
XX
OS Homo sapiens.
XX
PN WO200031266-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US027863.
XX
PR 25-NOV-1998; 98US-0109938P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Bringhurst FR, Takasu H, Gardella TJ, Potts JT;
XX
DR WPI; 2000-400076/34.
XX
PT Novel biologically active peptide comprising a parathyroid hormone
PT peptide derivative, useful for treating osteoporosis.
XX
PS Claim 6; Page 68; 75pp; English.
XX
CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC cells, initiating signal transduction. It has been identified that the
CC carboxyl terminal of PTH is important for PTH receptor binding, while the
CC amino terminal is important for signal transduction. Various PTH peptides

CC were produces with amino- and carboxy terminal modifications which had
CC varying PTH receptor activation properties and therefore downstream
CC signalling. Aberrant PTH activity has been implicated in a number of
CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC myeloma and epidermoid cancers of the head, neck and oesophagus. The
CC present sequence is a PTH peptide, with an Ala residue at position 1 and
CC an Arg residue at position 19. The Ala and Arg residues both improve
CC downstream signalling via phospholipase C (PLC) and ligand binding. The
CC present peptide may therefore be used as a PTH receptor agonist for the
CC treatment of the above mentioned disorders. In addition, the present
CC sequence would be suitable for fracture repair
XX
SQ Sequence 28 AA;

Query Match 71.1%; Score 59; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12
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Search completed: November 21, 2005, 16:38:10
Job time : 189 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:30:49 ; Search time 38 Seconds
(without alignments)
40.512 Million cell updates/sec

Title: SEQ-NEW
Perfect score: 83
Sequence: 1 avseiqlmhnlggggg 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59	71.1	115	2	A05091	parathyroid hormon
2	58	69.9	105	2	I51851	parathyroid hormon
3	56	67.5	115	1	PTHU	parathyroid hormon
4	56	67.5	115	1	PTPG	parathyroid hormon
5	55	66.3	115	1	PTBO	parathyroid hormon
6	53	63.9	119	2	A34937	parathyroid hormon
7	52	62.7	115	2	JC4202	parathyroid hormon
8	47	56.6	383	2	G69205	lipid-transfer pro
9	46	55.4	448	2	T43624	beta tubulin, temp
10	46	55.4	448	2	A21649	tubulin beta chain
11	46	55.4	448	2	T40019	beta tubulin - fis
12	46	55.4	456	2	S55661	hypothetical prote
13	45	54.2	395	2	S70637	tubulin beta chain
14	45	54.2	420	2	T22718	hypothetical prote
15	45	54.2	446	2	A27424	tubulin beta chain
16	45	54.2	450	2	S37177	tubulin beta chain
17	45	54.2	962	2	A84497	probable retroelem
18	44	53.0	196	2	E84638	probable RSZp22 sp
19	44	53.0	267	2	B82694	copper homeostasis
20	44	53.0	305	2	T04621	hypothetical prote
21	44	53.0	447	2	S17729	tubulin beta chain
22	44	53.0	447	2	S17730	tubulin beta chain
23	44	53.0	556	2	T06126	calcium-dependent
24	43	51.8	321	2	B25437	tubulin beta-2 cha
25	43	51.8	360	2	S18458	tubulin beta chain
26	43	51.8	437	2	I38369	beta-tubulin - hum
27	43	51.8	441	2	S05956	tubulin beta-2 cha
28	43	51.8	441	2	S45071	tubulin beta chain
29	43	51.8	443	2	S05968	tubulin beta-2 cha
30	43	51.8	444	1	UBHU5B	tubulin beta chain
31	43	51.8	444	2	D25437	tubulin beta-4 cha
32	43	51.8	444	2	S01713	tubulin beta-7 cha
33	43	51.8	444	2	A26561	tubulin beta chain
34	43	51.8	444	2	S18457	tubulin beta chain
35	43	51.8	444	2	S18456	tubulin beta chain
36	43	51.8	444	2	E25437	tubulin beta-5 cha
37	43	51.8	445	1	UBCHB	tubulin beta chain
38	43	51.8	445	1	UBPGB	tubulin beta chain
39	43	51.8	445	2	A25113	tubulin beta chain
40	43	51.8	445	2	B45794	tubulin beta chain
41	43	51.8	445	2	A24701	tubulin beta-3 cha
42	43	51.8	445	2	I50435	beta-1 tubulin - c
43	43	51.8	445	2	I38370	beta-tubulin - hum
44	43	51.8	445	2	S37144	tubulin beta chain
45	43	51.8	445	2	C25437	tubulin beta-3 cha
46	43	51.8	445	2	A54515	tubulin beta chain
47	43	51.8	445	2	T08726	tubulin beta chain
48	43	51.8	446	2	A27810	tubulin beta-2 cha
49	43	51.8	446	2	B27554	tubulin beta-5 cha
50	43	51.8	446	2	A48407	neural class-II be
51	43	51.8	447	2	S05429	tubulin beta chain
52	43	51.8	448	2	A45603	beta-tubulin - nem
53	43	51.8	448	2	S62125	tubulin beta chain
54	43	51.8	448	2	S53776	beta-tubulin isoty
55	43	51.8	449	2	A29161	tubulin beta-4 cha
56	43	51.8	449	2	T23201	hypothetical prote
57	43	51.8	450	2	A25437	tubulin beta-1 cha
58	43	51.8	450	2	T19788	hypothetical prote
59	43	51.8	452	2	T20194	hypothetical prote
60	43	51.8	453	2	S18597	tubulin beta chain
61	43	51.8	454	2	B27810	tubulin beta-3 cha
62	43	51.8	488	2	G65216	hypothetical 53.4
63	43	51.8	589	2	T19216	hypothetical prote
64	43	51.8	611	2	T19217	hypothetical prote
65	43	51.8	2174	2	E95965	hypothetical glyci
66	42	50.6	293	2	F75380	hypothetical prote
67	42	50.6	323	2	S20099	transforming prote
68	42	50.6	378	2	S72172	myoglobin - Japane
69	42	50.6	447	2	S43426	tubulin beta chain
70	42	50.6	1196	2	H85061	hypothetical prote
71	41	49.4	173	2	S53050	RNA binding protei
72	41	49.4	204	2	S02532	tubulin beta-1 cha
73	41	49.4	262	2	T51409	MADS box protein A
74	41	49.4	274	2	JC4053	chitinase (EC 3.2.
75	41	49.4	282	2	A25342	tubulin beta chain
76	41	49.4	342	1	TVMVM9	protein kinase (EC
77	41	49.4	354	1	TVMVMU	protein kinase (EC
78	41	49.4	374	1	TVMVHT	protein kinase (EC
79	41	49.4	374	1	TVMVM	protein kinase (EC
80	41	49.4	376	1	TVMV1M	protein kinase (EC
81	41	49.4	390	1	TVMSM	protein kinase (EC
82	41	49.4	441	2	E90136	tubulin beta subun
83	41	49.4	442	1	UBUTB	tubulin beta chain
84	41	49.4	442	2	S25182	tubulin beta 1 cha
85	41	49.4	442	2	S00683	tubulin beta-1 cha
86	41	49.4	442	2	S20908	tubulin beta chain
87	41	49.4	442	2	S05496	tubulin beta chain
88	41	49.4	443	2	S01769	tubulin beta-2 cha
89	41	49.4	443	2	S01768	tubulin beta-1 cha
90	41	49.4	443	2	S41470	tubulin beta chain
91	41	49.4	444	2	A45615	beta-tubulin - Pla
92	41	49.4	444	2	S31400	tubulin beta chain
93	41	49.4	444	2	A35885	tubulin beta chain
94	41	49.4	444	2	T18683	hypothetical prote
95	41	49.4	444	2	S35191	tubulin beta-1 cha
96	41	49.4	444	2	T15310	hypothetical prote
97	41	49.4	445	1	UBZQF	tubulin beta chain
98	41	49.4	445	2	S00743	tubulin beta chain
99	41	49.4	445	2	JA0048	tubulin beta-1 cha
100	41	49.4	445	2	JN0499	tubulin beta chain

ALIGNMENTS

RESULT 1
A05091
parathyroid hormone precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05091; A26806
R;Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
J. Biol. Chem. 259, 3320-3329, 1984
A;Reference number: A05091; MUID:84135846; PMID:6321505
A;Accession: A05091
A;Molecule type: DNA
A;Residues: 1-115 <HEI>
A;Cross-references: UNIPROT:P04089; UNIPARC:UPI000013290C; GB:K01268; NID:g206483; PIDN:
A;Note: the authors translated the codon GAA for residue 87 as Asp
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: A26806
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: UNIPARC:UPI000013290C; GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA291
C;Genetics:
A;Introns: 29/3
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;30-64/Domain: parathyroid hormone homology <PTH>

  Query Match 71.1%; Score 59; DB 2; Length 115;
  Best Local Similarity 100.0%; Pred. No. 0.022;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
||||||||||||
Db 32 AVSEIQLMHNLG 43

RESULT 2
I51851
parathyroid hormone - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I51851
R;Schmelzer, H.
Adv. Gene Technol. 21, 228-229, 1984
A;Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A;Reference number: I51851
A;Accession: I51851
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-105 <RES>
A;Cross-references: UNIPARC:UPI0000170AE0; GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:
C;Genetics:
A;Gene: PTH
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;20-54/Domain: parathyroid hormone homology <PTH>

  Query Match 69.9%; Score 58; DB 2; Length 105;
  Best Local Similarity 91.7%; Pred. No. 0.029;
  Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
|:||||||||||
Db 22 AISEIQLMHNLG 33

RESULT 3
PTHU
parathyroid hormone precursor [validated] - human
N;Alternate names: proparathyroid hormone
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410; I38
R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
A;Title: Nucleotide sequence of the human parathyroid hormone gene.
A;Reference number: A19339; MUID:83169834; PMID:6220408
A;Accession: A19339
A;Molecule type: DNA
A;Residues: 1-115 <VAS>
A;Cross-references: UNIPROT:P01270; UNIPARC:UPI000013290A; GB:J00301; NID:g190702; PIDN:
R;Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.
Biol. Chem. Hoppe-Seyler 375, 821-824, 1994
A;Title: Purification of meprin from human kidney and its role in parathyroid hormone deg
A;Reference number: S53790; MUID:95225988; PMID:7710697
A;Accession: S53790
A;Molecule type: protein
A;Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>
A;Cross-references: UNIPARC:UPI00001734E1; UNIPARC:UPI00001734E2; UNIPARC:UPI00001734E3
A;Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occurrec
R;Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974
A;Title: Structural analysis of human proparathyroid hormone by a new microsequencing app
A;Reference number: A93169; MUID:74174967; PMID:4833516
A;Accession: A93169
A;Molecule type: protein
A;Residues: 26-37 <JAC>
A;Cross-references: UNIPARC:UPI00001734E4
R;Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.T.
Eur. J. Biochem. 205, 311-319, 1992
A;Title: Isolation and characterization of two biologically active O-glycosylated forms c
ation.
A;Reference number: S21199; MUID:92209518; PMID:1555591
A;Accession: S21199
A;Molecule type: protein
A;Residues: 32-114,'N' <OLS>
A;Cross-references: UNIPARC:UPI00001734E5
A;Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation;
R;Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L.H.;
Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974
A;Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid h
A;Reference number: A93789; MUID:74111656; PMID:4521809
A;Accession: A93789
A;Molecule type: protein
A;Residues: 32-68 <NIA>
A;Cross-references: UNIPARC:UPI000002DA05
R;Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972
A;Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residues 1-
A;Reference number: A93783; MUID:73070429; PMID:4509319
A;Accession: A93783
A;Molecule type: protein
A;Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <BRE>
A;Cross-references: UNIPARC:UPI00001734E6
A;Note: this sequence was determined by sequenator and mass spectroscopic identification
R;Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 14, 1842-1847, 1975
A;Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
A;Reference number: A90387; MUID:75146516; PMID:1125201
A;Accession: A90387
A;Molecule type: protein
A;Residues: 52-75 <KE3>
A;Cross-references: UNIPARC:UPI00001734E7
R;Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 17, 5723-5729, 1978
A;Title: Complete amino acid sequence of human parathyroid hormone.
A;Reference number: A90426; MUID:79082855; PMID:728431
A;Accession: A90426
A;Molecule type: protein
A;Residues: 61-106,'D',108-115 <KEU>
A;Cross-references: UNIPARC:UPI00001734E8
R;Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.H
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-1

A;Reference number: A94410
A;Accession: A94410
A;Molecule type: protein
A;Residues: 75-100 <KE2>
A;Cross-references: UNIPARC:UPI00001734E9
R;Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J
Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
A;Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum
A;Reference number: A91660; MUID:75059220; PMID:4474131
A;Contents: annotation; synthesis of residues 32-65
A;Note: the biologically active amino-terminal 34 residues of parathyroid hormone were s
at renal adenylate cyclase assay and with the bovine hormone's active region in the chic
R;Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel,
Helv. Chim. Acta 56, 470-473, 1973
A;Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
A;Reference number: A91635; MUID:73227467; PMID:4721748
A;Contents: annotation; synthesis of residues 32-65
A;Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined
into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
R;Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
A;Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
A;Reference number: I38342; MUID:82150870; PMID:6950381
A;Accession: I38342
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: UNIPARC:UPI000013290A; EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PID
C;Genetics:
A;Gene: GDB:PTH
A;Cross-references: GDB:119522; OMIM:168450
A;Map position: 11p15.2-11p15.1
A;Introns: 29/2
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: factor in homeostatic control of plasma calcium and phosphate; released b
counter to calcitonin
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland; plasma
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 67.5%; Score 56; DB 1; Length 115;
Best Local Similarity 91.7%; Pred. No. 0.067;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
:||||||||||||
Db 32 SVSEIQLMHNLG 43

RESULT 4
PTPG
parathyroid hormone precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: B26806; A90390; A90376; A01535
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: B26806
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: UNIPROT:P01269; UNIPARC:UPI000013290B; GB:X05722; GB:Y00409; NID:g18
R;Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Biochemistry 14, 3631-3635, 1975
A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial amino
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Accession: A90390
A;Molecule type: protein
A;Residues: 26-115 <CHU>
A;Cross-references: UNIPARC:UPI00001592DF
R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J
Biochemistry 13, 1994-1999, 1974
A;Title: The amino acid sequence of porcine parathyroid hormone.
A;Reference number: A90376; MUID:74253317; PMID:4840833
A;Accession: A90376
A;Molecule type: protein
A;Residues: 32-109 <SAU>
A;Cross-references: UNIPARC:UPI00001734E0
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormon
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: calcium; hormone; parathyroid gland
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 67.5%; Score 56; DB 1; Length 115;
Best Local Similarity 91.7%; Pred. No. 0.067;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
:||||||||||||
Db 32 SVSEIQLMHNLG 43

RESULT 5
PTBO
parathyroid hormone precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534
R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.
Gene 28, 319-329, 1984
A;Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroid h
A;Reference number: A24949; MUID:84262483; PMID:6086460
A;Accession: A24949
A;Molecule type: DNA
A;Residues: 1-115 <WEA>
A;Cross-references: UNIPROT:P01268; UNIPARC:UPI0000132907; GB:K01938
R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr.,
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979
A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid horm
A;Reference number: A93835; MUID:80056617; PMID:388425
A;Accession: A93835
A;Molecule type: DNA
A;Residues: 1-115 <KRO>
A;Cross-references: UNIPARC:UPI0000132907; GB:V00106; GB:J00023; NID:g84; PIDN:CAA23439.
A;Note: the authors translated the codon GAA for residue 50 as Gly
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.V.
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974
A;Title: The N-terminal amino-acid sequence of bovine proparathyroid hormone.
A;Reference number: A93793; MUID:74142666; PMID:4522780
A;Accession: A93793
A;Molecule type: protein
A;Residues: 26-115 <HAM>
A;Cross-references: UNIPARC:UPI00001734DF
R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; Pott
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970
A;Title: The amino acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162; PMID:5531031
A;Accession: A91648
A;Molecule type: protein
A;Residues: 32-115 <NIA>
A;Cross-references: UNIPARC:UPI00000473E4
R;Brewer Jr., H.B.; Ronan, R.
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970

```
A;Title: Bovine parathyroid hormone: amino acid sequence.
A;Reference number: A93773; MUID:71063634; PMID:5275384
A;Accession: A93773
A;Molecule type: protein
A;Residues: 32-115 <BRE>
A;Cross-references: UNIPARC:UPI00000473E4
R;Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.;
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
A;Title: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyr
A;Reference number: A93776; MUID:71091588; PMID:4322265
A;Contents: annotation; synthesis of residues 32-65
A;Note: the synthetic peptide was active in vivo and in vitro
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormon
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Contents: annotation
R;Weaver, C.A.; Gordon, D.F.
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
A;Title: introduction by molecular cloning of artifactual inverted sequences at the 5' t
A;Reference number: I45975; MUID:82037785; PMID:6170060
A;Accession: I45975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE2>
A;Cross-references: UNIPARC:UPI0000132907; GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:
R;Weaver, C.A.; Gordon, D.F.
Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: I45976; MUID:83105964; PMID:6185374
A;Accession: I45976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE3>
A;Cross-references: UNIPARC:UPI0000132907; GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:
C;Genetics:
A;Gene: PTH
A;Introns: 29/2
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-115/Product: proparathyroid hormone #status experimental <PMAT>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>

  Query Match             66.3%;  Score 55;  DB 1;  Length 115;
  Best Local Similarity   91.7%;  Pred. No. 0.096;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              |||||| |||||
Db         32 AVSEIQFMHNLG 43


RESULT 6
A34937
parathyroid hormone precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: A34937; I50411
R;Russell, J.; Sherwood, L.M.
Mol. Endocrinol. 3, 325-331, 1989
A;Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyro
A;Reference number: A34937; MUID:89219100; PMID:2710135
A;Accession: A34937
A;Molecule type: mRNA
A;Residues: 1-119 <RUS>
A;Cross-references: UNIPROT:P15743; UNIPARC:UPI0000132909; GB:M31604; NID:g212767; PIDN:
R;Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.
J. Bone Miner. Res. 3, 689-698, 1988
A;Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.
A;Reference number: I50411; MUID:89284968; PMID:3251402
A;Accession: I50411
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-119 <KHO>
A;Cross-references: UNIPARC:UPI0000132909; GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-31/Domain: propeptide #status predicted <PRO>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-119/Product: parathyroid hormone #status predicted <MAT>

  Query Match             63.9%;  Score 53;  DB 2;  Length 119;
  Best Local Similarity   83.3%;  Pred. No. 0.21;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :|||:|||||||
Db         32 SVSEMQLMHNLG 43


RESULT 7
JC4202
parathyroid hormone precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C;Accession: JC4202
R;Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.C.
Gene 160, 241-243, 1995
A;Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein and p
A;Reference number: JC4201; MUID:95369696; PMID:7642102
A;Accession: JC4202
A;Molecule type: mRNA
A;Residues: 1-115 <ROS>
A;Cross-references: UNIPROT:P52212; UNIPARC:UPI0000132908; GB:U15662; NID:g558915; PIDN:A
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-31/Domain: signal sequence #status predicted <SIG>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status predicted <MAT>

  Query Match             62.7%;  Score 52;  DB 2;  Length 115;
  Best Local Similarity   83.3%;  Pred. No. 0.29;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :||||| |||||
Db         32 SVSEIQFMHNLG 43


RESULT 8
G69205
lipid-transfer protein (sterol or nonspecific) - Methanobacterium thermoautotrophicum (st
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69205
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; B
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.,
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69205
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-383 <MTH>
A;Cross-references: UNIPROT:O26884; UNIPARC:UPI00000664E4; GB:AE000857; GB:AE000666; NID
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH793

  Query Match             56.6%;  Score 47;  DB 2;  Length 383;
  Best Local Similarity   57.1%;  Pred. No. 6.9;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy          3 SEIQLMHNLGGGGG 16
              :|| : ||:|| ||
Db        361 AEIGMTHNIGGTGG 374
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RESULT 9
T43624
beta tubulin, temperature sensitive - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43624
R;Radcliffe, P.; Hirata, D.; Childs, D.; Vardy, L.; Toda, T.
Mol. Biol. Cell 9, 1757-1771, 1998
A;Title: Identification of novel temperature-sensitive lethal alleles in essential beta-
A;Reference number: Z22579; MUID:98324923; PMID:9658169
A;Accession: T43624
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-448 <RAD>
A;Cross-references: UNIPROT:P05219; UNIPARC:UPI0000168807; EMBL:AF042828; PIDN:AAC21455.
A;Experimental source: strain 972
C;Genetics:
A;Gene: nda3
A;Map position: 2
A;Introns: 4/3; 21/2; 35/2; 53/3; 349/1
C;Superfamily: tubulin

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  Query Match             55.4%;  Score 46;  DB 2;  Length 448;
  Best Local Similarity   56.2%;  Pred. No. 12;
  Matches    9;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGGGG 16
              |:   || |:|||| |
Db        129 ALQGFQLTHSLGGGTG 144
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RESULT 10
A21649
tubulin beta chain - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C;Accession: A21649
R;Hiraoka, Y.; Toda, T.; Yanagida, M.
Cell 39, 349-358, 1984
A;Title: The NDA3 gene of fission yeast encodes beta-tubulin: a cold-sensitive nda3 muta
A;Reference number: A21649; MUID:85048945; PMID:6094012
A;Accession: A21649
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <HIR>
A;Cross-references: UNIPROT:P05219; UNIPARC:UPI00001691C0; GB:M10347; NID:g173522; PIDN:
C;Superfamily: tubulin

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  Query Match             55.4%;  Score 46;  DB 2;  Length 448;
  Best Local Similarity   56.2%;  Pred. No. 12;
  Matches    9;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGGGG 16
              |:   || |:|||| |
Db        129 ALQGFQLTHSLGGGTG 144
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RESULT 11
T40019
beta tubulin - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40019; T43623
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21899
A;Accession: T40019
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-448 <WOO>
A;Cross-references: UNIPROT:P05219; UNIPARC:UPI0000136A39; EMBL:AL031743; PIDN:CAA21099.1
A;Experimental source: strain 972h-; cosmid c26H8
R;Radcliffe, P.; Hirata, D.; Childs, D.; Vardy, L.; Toda, T.
Mol. Biol. Cell 9, 1757-1771, 1998
A;Title: Identification of novel temperature-sensitive lethal alleles in essential beta-t
A;Reference number: Z22579; MUID:98324923; PMID:9658169
A;Accession: T43623
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-448 <RAD>
A;Cross-references: UNIPARC:UPI0000136A39; EMBL:AF042827; PIDN:AAC21454.1
A;Experimental source: strain 972
C;Genetics:
A;Gene: nda3; SPBC26H8.07c
A;Map position: 2
A;Introns: 4/3; 21/2; 35/2; 53/3; 349/1
C;Superfamily: tubulin

```
  Query Match             55.4%;  Score 46;  DB 2;  Length 448;
  Best Local Similarity   56.2%;  Pred. No. 12;
  Matches    9;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGGGG 16
              |:   || |:|||| |
Db        129 ALQGFQLTHSLGGGTG 144
```

RESULT 12
S55661
hypothetical protein 66 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55661
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55661
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-456 <TEL>
A;Cross-references: UNIPROT:Q66668; UNIPARC:UPI00000F0F2B; GB:U20824; NID:g695172; PIDN:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

```
  Query Match             55.4%;  Score 46;  DB 2;  Length 456;
  Best Local Similarity   63.6%;  Pred. No. 12;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 QLMHNLGGGGG 16
              :: | ||||||
Db          8 EIFHRLGGGGG 18
```

RESULT 13
S70637
tubulin beta chain - Hexamita sp. (strain ATCC 50330) (fragment)
C;Species: Hexamita sp.
A;Variety: ATCC 50330
C;Date: 21-Apr-1997 #sequence_revision 21-Apr-1997 #text_change 07-Dec-1999
C;Accession: S70637
R;Keeling, P.J.; Doolittle, W.F.
EMBO J. 15, 2285-2290, 1996
A;Title: A non-canonical genetic code in an early diverging eukaryotic lineage.
A;Reference number: S70634; MUID:96208514; PMID:8641293
A;Accession: S70637
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-395 <KEE>
A;Cross-references: UNIPARC:UPI000007A51C; EMBL:U29441; NID:g1322213; PIDN:AAC47210.1; P
A;Experimental source: ATCC 50330

```
A;Note: the sequence of residues 388-395 and the corresponding nucleic acid sequence are
C;Genetics:
A;Genetic code: SGC5
C;Superfamily: tubulin

  Query Match             54.2%;  Score 45;  DB 2;  Length 395;
  Best Local Similarity   72.7%;  Pred. No. 15;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QLMHNLGGGGG 16
              ||:|:|||| |
Db        119 QLVHSLGGGTG 129


RESULT 14
T22718
hypothetical protein T04H1.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22718; T24481
R;Harris, B.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19604
A;Accession: T22718
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-420 <WIL>
A;Cross-references: UNIPROT:Q20823; UNIPARC:UPI0000061142; EMBL:Z78198; PIDN:CAB01575.1;
A;Experimental source: clone F55C5
R;Harris, B.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19896
A;Accession: T24481
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-420 <WI2>
A;Cross-references: UNIPARC:UPI0000061142; EMBL:Z78200; PIDN:CAB01587.1; GSPDB:GN00023;
A;Experimental source: clone T04H1
C;Genetics:
A;Gene: CESP:T04H1.9
A;Map position: 5
A;Introns: 56/1; 120/1; 224/1; 379/1
C;Superfamily: tubulin

  Query Match             54.2%;  Score 45;  DB 2;  Length 420;
  Best Local Similarity   72.7%;  Pred. No. 16;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QLMHNLGGGGG 16
              ||:|:|||| |
Db        134 QLIHSLGGGTG 144


RESULT 15
A27424
tubulin beta chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27424
R;Murphy, D.B.; Wallis, K.T.; Machlin, P.S.; Ratrie III, H.; Cleveland, D.W.
J. Biol. Chem. 262, 14305-14312, 1987
A;Title: The sequence and expression of the divergent beta-tubulin in chicken erythrocyt
A;Reference number: A27424; MUID:88007687; PMID:2888766
A;Accession: A27424
A;Molecule type: mRNA
A;Residues: 1-446 <MUR>
A;Cross-references: UNIPROT:P09207; UNIPARC:UPI0000136A03; GB:J02828; NID:g212833; PIDN:
C;Superfamily: tubulin
C;Keywords: microtubule

  Query Match             54.2%;  Score 45;  DB 2;  Length 446;
  Best Local Similarity   72.7%;  Pred. No. 17;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QLMHNLGGGGG 16
              ||:|:|||| |
Db        134 QLIHSLGGGTG 144


RESULT 16
S37177
tubulin beta chain - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37177
R;Mita, K.
submitted to the EMBL Data Library, September 1993
A;Reference number: S37177
A;Accession: S37177
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-450 <MIT>
A;Cross-references: UNIPROT:P41385; UNIPARC:UPI0000136A12; EMBL:X74951; NID:g402173; PIDN
C;Superfamily: tubulin

  Query Match             54.2%;  Score 45;  DB 2;  Length 450;
  Best Local Similarity   72.7%;  Pred. No. 17;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QLMHNLGGGGG 16
              ||:|:|||| |
Db        134 QLVHSLGGGTG 144


RESULT 17
A84497
probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: A84497
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84497
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-962 <STO>
A;Cross-references: UNIPROT:Q9ZQM1; UNIPARC:UPI00000AB92C; GB:AE002093; NID:g4263654; PI
C;Genetics:
A;Gene: At2g11230
A;Map position: 2

  Query Match             54.2%;  Score 45;  DB 2;  Length 962;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 IQLMHNLGGGGG 16
              :|| | ||| ||
Db        656 VQLTHRLGGRGG 667


RESULT 18
E84638
probable RSZp22 splicing factor [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84638
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
```

```
A;Accession: E84638
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196 <STO>
A;Cross-references: UNIPROT:Q9SJA6; UNIPARC:UPI000000C588; GB:AE002093; NID:g4572679; PI
C;Genetics:
A;Gene: At2g24590
A;Map position: 2
C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology

  Query Match             53.0%;  Score 44;  DB 2;  Length 196;
  Best Local Similarity   58.3%;  Pred. No. 10;
  Matches    7;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 IQLMHNLGGGGG 16
              ::  || |||||
Db         66 VEQSHNRGGGGG 77


RESULT 19
B82694
copper homeostasis protein XF1341 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82694
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82694
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <SIM>
A;Cross-references: UNIPROT:Q9PDN8; UNIPARC:UPI00000C26D0; GB:AE003966; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laign
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1341

  Query Match             53.0%;  Score 44;  DB 2;  Length 267;
  Best Local Similarity   63.6%;  Pred. No. 14;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 IQLMHNLGGGG 15
              ::| | |||||
Db         49 VELCHGLGGGG 59


RESULT 20
T04621
hypothetical protein F20O9.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04621
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, October 1998
A;Reference number: Z15380
A;Accession: T04621
A;Molecule type: DNA
A;Residues: 1-305 <BEV>
A;Cross-references: UNIPROT:O49459; UNIPARC:UPI00000A2285; EMBL:AL021749
A;Experimental source: cultivar Columbia; BAC clone F20O9
C;Genetics:
A;Map position: 4
A;Introns: 50/3; 114/1
A;Note: F20O9.190

  Query Match             53.0%;  Score 44;  DB 2;  Length 305;
  Best Local Similarity   77.8%;  Pred. No. 16;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLGGGGG 16
              :| ||||||
Db        241 LHGLGGGGG 249


Search completed: November 21, 2005, 16:38:53
Job time : 40 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:31:04 ; Search time 234 Seconds
(without alignments)
48.241 Million cell updates/sec

Title: SEQ-NEW
Perfect score: 83
Sequence: 1 avseiqlmhnlggggg 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59	71.1	31	2	Q91Y90_PERMA	Q91y90 peromyscus
2	59	71.1	31	2	Q91Y91_PERPL	Q91y91 peromyscus
3	59	71.1	105	2	Q80WZ2_RAT	Q80wz2 rattus norv
4	59	71.1	115	1	PTHY_RAT	P04089 rattus norv
5	59	71.1	115	2	Q9Z0L6_MOUSE	Q9z0l6 mus musculu
6	56	67.5	86	2	Q9N1V0_HORSE	Q9n1v0 equus cabal
7	56	67.5	115	1	PTHY_HUMAN	P01270 homo sapien
8	56	67.5	115	1	PTHY_MACFA	Q9xt35 macaca fasc
9	56	67.5	115	1	PTHY_PIG	P01269 sus scrofa
10	56	67.5	115	2	Q4VB48_HUMAN	Q4vb48 homo sapien
11	55	66.3	102	2	Q5TLZ1_BRARE	Q5tlz1 brachydanio
12	55	66.3	102	2	Q6WQ25_BRARE	Q6wq25 brachydanio
13	55	66.3	115	1	PTHY_BOVIN	P01268 bos taurus
14	53	63.9	119	1	PTHY_CHICK	P15743 gallus gall
15	52	62.7	115	1	PTHY_CANFA	P52212 canis famil
16	52	62.7	115	1	PTHY_FELCA	Q9gl67 felis silve
17	50	60.2	394	2	Q8TVL1_METKA	Q8tvl1 methanopyru
18	49	59.0	885	2	Q55GS9_DICDI	Q55gs9 dictyosteli
19	48	57.8	140	2	Q5SXZ6_MOUSE	Q5sxz6 mus musculu
20	48	57.8	190	2	Q5SXZ5_MOUSE	Q5sxz5 mus musculu
21	48	57.8	373	2	Q6WNZ3_9EUKA	Q6wnz3 trichomitus
22	48	57.8	380	2	Q6WNZ0_9EUKA	Q6wnz0 monocercomo
23	48	57.8	380	2	Q6WNZ1_9EUKA	Q6wnz1 monocercomo
24	48	57.8	380	2	Q6WNZ2_9EUKA	Q6wnz2 trichomitus
25	48	57.8	380	2	Q6WNZ4_TRIFO	Q6wnz4 tritrichomo
26	48	57.8	380	2	Q6WNZ8_9EUKA	Q6wnz8 tetratricho
27	48	57.8	380	2	Q6WNZ9_9EUKA	Q6wnz9 tetratricho
28	48	57.8	380	2	Q6WP00_9EUKA	Q6wp00 tetratricho
29	48	57.8	380	2	Q6WP01_9EUKA	Q6wp01 hypotrichom
30	48	57.8	380	2	Q6WP02_9EUKA	Q6wp02 hypotrichom
31	48	57.8	380	2	Q6WP03_9EUKA	Q6wp03 hypotrichom
32	48	57.8	387	2	Q86ZX6_9FUNG	Q86zx6 karlingiomy
33	48	57.8	398	2	Q8CB15_MOUSE	Q8cb15 mus musculu
34	48	57.8	1192	2	Q5ZKU4_CHICK	Q5zku4 gallus gall
35	48	57.8	1198	2	Q80UK8_MOUSE	Q80uk8 mus musculu
36	48	57.8	1198	2	Q6PCY7_MOUSE	Q6pcy7 mus musculu
37	48	57.8	1202	2	Q6ZPU6_MOUSE	Q6zpu6 mus musculu
38	48	57.8	1204	2	Q9H0H0_HUMAN	Q9h0h0 homo sapien
39	48	57.8	1209	2	Q9ULD3_HUMAN	Q9uld3 homo sapien
40	47	56.6	309	2	Q74CW5_GEOSL	Q74cw5 geobacter s
41	47	56.6	383	1	Y793_METTH	O26884 methanobact
42	47	56.6	552	2	Q4SIA2_TETNG	Q4sia2 tetraodon n
43	47	56.6	829	2	Q7QA69_ANOGA	Q7qa69 anopheles g
44	47	56.6	1175	2	Q6NS25_XENLA	Q6ns25 xenopus lae
45	47	56.6	1180	2	Q501R5_XENTR	Q501r5 xenopus tro
46	47	56.6	1254	2	Q8IRT7_DROME	Q8irt7 drosophila
47	47	56.6	1266	2	Q9W4Q4_DROME	Q9w4q4 drosophila
48	47	56.6	2126	2	Q7PUB0_ANOGA	Q7pub0 anopheles g
49	46.5	56.0	343	2	Q5TQE7_ANOGA	Q5tqe7 anopheles g
50	46	55.4	139	2	Q8X188_PAXIN	Q8x188 paxillus in
51	46	55.4	398	2	Q76HZ6_9METZ	Q76hz6 dicyema sp.
52	46	55.4	445	1	TBB2_SUIBO	Q8j1r4 suillus bov
53	46	55.4	448	1	TBB_SCHPO	P05219 schizosacch
54	46	55.4	452	2	Q55MJ4_CRYNE	Q55mj4 cryptococcu
55	46	55.4	452	2	Q5K876_CRYNE	Q5k876 cryptococcu
56	46	55.4	456	2	Q66668_9GAMA	Q66668 equid herpe
57	46	55.4	477	2	Q6IEH9_FUGRU	Q6ieh9 fugu rubrip
58	46	55.4	1535	2	Q6K9S9_ORYSA	Q6k9s9 oryza sativ
59	45	54.2	99	2	Q6WQ24_BRARE	Q6wq24 brachydanio
60	45	54.2	138	2	Q6ZIR5_ORYSA	Q6zir5 oryza sativ
61	45	54.2	152	2	Q27117_TRIVA	Q27117 trichomonas
62	45	54.2	152	2	Q27118_TRIVA	Q27118 trichomonas
63	45	54.2	165	2	Q69MS6_ORYSA	Q69ms6 oryza sativ
64	45	54.2	211	2	Q67UK6_ORYSA	Q67uk6 oryza sativ
65	45	54.2	289	2	Q533X3_ORENI	Q533x3 oreochromis
66	45	54.2	291	2	Q4P3J3_USTMA	Q4p3j3 ustilago ma
67	45	54.2	341	2	Q726K6_DESVH	Q726k6 desulfovibr
68	45	54.2	365	2	Q84R44_ORYSA	Q84r44 oryza sativ
69	45	54.2	380	2	Q6WNY9_9EUKA	Q6wny9 hexamita in
70	45	54.2	388	2	Q86ZX2_9FUNG	Q86zx2 nowakowskie
71	45	54.2	395	2	Q25165_SPIBA	Q25165 spironucleu
72	45	54.2	415	2	Q8AYD9_MORSA	Q8ayd9 morone saxa
73	45	54.2	426	2	Q20823_CAEEL	Q20823 caenorhabdi
74	45	54.2	444	2	Q76DW0_9EUKA	Q76dw0 trichonymph
75	45	54.2	444	2	Q76DW1_9EUKA	Q76dw1 trichonymph
76	45	54.2	445	2	Q7T0Q9_XENLA	Q7t0q9 xenopus lae
77	45	54.2	446	1	TBB6_CHICK	P09207 gallus gall
78	45	54.2	446	2	Q27116_TRIVA	Q27116 trichomonas
79	45	54.2	450	1	TBB_BOMMO	P41385 bombyx mori
80	45	54.2	460	2	Q4RVA6_TETNG	Q4rva6 tetraodon n
81	45	54.2	693	2	Q5A586_CANAL	Q5a586 candida alb
82	45	54.2	962	2	Q9ZQM1_ARATH	Q9zqm1 arabidopsis
83	44.5	53.6	364	2	Q6ZHF2_ORYSA	Q6zhf2 oryza sativ
84	44	53.0	91	2	Q6W9J4_FUGRU	Q6w9j4 fugu rubrip
85	44	53.0	162	2	Q9AV00_ORYSA	Q9av00 oryza sativ
86	44	53.0	196	2	Q9SJA6_ARATH	Q9sja6 arabidopsis
87	44	53.0	201	2	Q53N79_ORYSA	Q53n79 oryza sativ
88	44	53.0	228	2	Q6ND70_RHOPA	Q6nd70 rhodopseudo
89	44	53.0	267	1	CUTC_XYLFA	Q9pdn8 xylella fas
90	44	53.0	305	2	O49459_ARATH	O49459 arabidopsis
91	44	53.0	310	1	PIM1_BRARE	Q9yhz5 brachydanio
92	44	53.0	310	2	Q5C8G1_9PEZI	Q5c8g1 valsa cerat
93	44	53.0	310	2	Q6DI52_BRARE	Q6di52 brachydanio
94	44	53.0	310	2	Q7ZVJ5_BRARE	Q7zvj5 brachydanio
95	44	53.0	310	2	Q8JFW9_BRARE	Q8jfw9 brachydanio
96	44	53.0	320	2	Q855I5_9CAUD	Q855i5 mycobacteri
97	44	53.0	350	2	Q67RA0_SYMTH	Q67ra0 symbiobacte
98	44	53.0	357	2	Q6ZDR4_ORYSA	Q6zdr4 oryza sativ
99	44	53.0	371	2	Q60TD0_CAEBR	Q60td0 caenorhabdi
100	44	53.0	396	2	Q6BUW8_DEBHA	Q6buw8 debaryomyce

ALIGNMENTS

```
RESULT 1
Q91Y90_PERMA
ID   Q91Y90_PERMA PRELIMINARY;      PRT;    31 AA.
AC   Q91Y90;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Parathyroid hormone (Fragment).
GN   Name=Pth;
OS   Peromyscus maniculatus (Deer mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Sigmodontinae; Peromyscus.
OX   NCBI_TaxID=10042;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Prince K.L., Dewey M.J.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF382953; AAK63072.1; -; Genomic_DNA.
DR   HSSP; P01270; 1ZWB.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
FT   NON_TER       1      1
FT   NON_TER      31     31
SQ   SEQUENCE   31 AA;  3461 MW;  A208B0E772B9B55B CRC64;

  Query Match             71.1%;  Score 59;  DB 2;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db         13 AVSEIQLMHNLG 24


RESULT 2
Q91Y91_PERPL
ID   Q91Y91_PERPL PRELIMINARY;      PRT;    31 AA.
AC   Q91Y91;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Parathyroid hormone (Fragment).
GN   Name=Pth;
OS   Peromyscus polionotus (Oldfield mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Sigmodontinae; Peromyscus.
OX   NCBI_TaxID=42413;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Prince K.L., Dewey M.J.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF382952; AAK63071.1; -; Genomic_DNA.
DR   HSSP; P01270; 1ZWB.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
FT   NON_TER       1      1
FT   NON_TER      31     31
SQ   SEQUENCE   31 AA;  3461 MW;  A208B0E772B9B55B CRC64;

  Query Match             71.1%;  Score 59;  DB 2;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db         13 AVSEIQLMHNLG 24


RESULT 3
Q80WZ2_RAT
ID   Q80WZ2_RAT  PRELIMINARY;      PRT;   105 AA.
AC   Q80WZ2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothalamic parathyroid hormone.
GN   Name=PTH-(1-84);
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA   Nutley M.T., Parimi S.A., Harvey S.;
RT   "Sequence analysis of hypothalamic parathyroid hormone messenger
RT   ribonucleic acid.";
RL   Endocrinology 136:5600-5607(1995).
DR   EMBL; S80127; AAP32220.1; -; mRNA.
DR   HSSP; P01270; 1ZWB.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
SQ   SEQUENCE   105 AA;  11684 MW;  18EE71B3F1CF5F70 CRC64;

  Query Match             71.1%;  Score 59;  DB 2;  Length 105;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db         22 AVSEIQLMHNLG 33


RESULT 4
PTHY_RAT
ID   PTHY_RAT       STANDARD;      PRT;   115 AA.
AC   P04089; Q63473;
DT   01-NOV-1986 (Rel. 03, Created)
DT   01-NOV-1986 (Rel. 03, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=Pth;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84135846; PubMed=6321505;
RA   Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
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RT   "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
RT   gene and deduced amino acid sequence of rat preproparathyroid
RT   hormone.";
RL   J. Biol. Chem. 259:3320-3329(1984).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 10-115.
RC   TISSUE=Parathyroid;
RA   Schmelzer H.J., Gross G., Mayer H.;
RT   "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
RT   hormone.";
RL   Adv. Gene Technol. 21:228-229(1984).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 32-115.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
RX   MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
RA   Nutley M.T., Parimi S.A., Harvey S.;
RT   "Sequence analysis of hypothalamic parathyroid hormone messenger
RT   ribonucleic acid.";
RL   Endocrinology 136:5600-5607(1995).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Hypothalamus and parathyroid gland.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; K01268; AAA41979.1; -; Genomic_DNA.
DR   EMBL; X05721; CAA29192.1; -; mRNA.
DR   EMBL; M54875; AAA57156.1; -; mRNA.
DR   EMBL; S80127; -; NOT_ANNOTATED_CDS; mRNA.
DR   PIR; A05091; A05091.
DR   HSSP; P01270; 1ZWB.
DR   Ensembl; ENSRNOG00000014318; Rattus norvegicus.
DR   RGD; 3440; Pth.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003626; PTH_related.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD013225; PTH_related; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
FT   CONFLICT     18     18       C -> Y (in Ref. 3).
FT   CONFLICT     23     23       A -> T (in Ref. 3).
FT   CONFLICT     33     33       V -> I (in Ref. 3).
FT   CONFLICT     62     62       V -> G (in Ref. 3).
SQ   SEQUENCE   115 AA;  12722 MW;  7B434CFCA528B230 CRC64;

  Query Match             71.1%;  Score 59;  DB 1;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db         32 AVSEIQLMHNLG 43
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RESULT 5
Q9Z0L6_MOUSE
ID   Q9Z0L6_MOUSE PRELIMINARY;      PRT;   115 AA.
AC   Q9Z0L6;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Parathyroid hormone precursor.
GN   Name=Pth;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/Sv;
RA   Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.;
RT   "Cloning of the murine gene encoding parathyroid hormone: genomic
RT   organization and nucleotide sequence.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thyroid;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF066075; AAC99656.1; -; Genomic_DNA.
DR   EMBL; BC099456; AAH99456.1; -; mRNA.
DR   HSSP; P01270; 1ZWB.
DR   Ensembl; ENSMUSG00000059077; Mus musculus.
DR   MGI; MGI:97799; Pth.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005179; F:hormone activity; IDA.
DR   GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Signal.
FT   SIGNAL        1     25       Potential.
FT   CHAIN        32    115       parathyroid hormone.
SQ   SEQUENCE   115 AA;  12825 MW;  DA43FABBCB4E2FD9 CRC64;
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  Query Match             71.1%;  Score 59;  DB 2;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db         32 AVSEIQLMHNLG 43


RESULT 6
Q9N1V0_HORSE
ID   Q9N1V0_HORSE PRELIMINARY;      PRT;    86 AA.
AC   Q9N1V0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Parathyroid hormone (Fragment).
GN   Name=PTH;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;
RA   Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Bowling A.T., Murray J.D.;
RT   "A comparative gene map of the horse (Equus caballus).";
RL   Genome Res. 9:1239-1249(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Shiue Y.-L., Caetano A.R., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Murray J.D., Bowling A.T.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF134233; AAF62347.1; -; Genomic_DNA.
DR   HSSP; P01270; 1ET1.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   86 AA;  9805 MW;  253184EA681A2022 CRC64;

  Query Match             67.5%;  Score 56;  DB 2;  Length 86;
  Best Local Similarity   91.7%;  Pred. No. 0.48;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :|||||||||||
Db          3 SVSEIQLMHNLG 14


RESULT 7
PTHY_HUMAN
ID   PTHY_HUMAN     STANDARD;      PRT;   115 AA.
AC   P01270;
DT   21-JUL-1986 (Rel. 01, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).
GN   Name=PTH;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82150870; PubMed=6950381;
RA   Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;
RT   "Nucleotide sequence of cloned cDNAs encoding human preproparathyroid
RT   hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83169834; PubMed=6220408;
RA   Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J., Hendy G.N.,
RA   Potts J.T. Jr., Rich A., Kronenberg H.M.;
RT   "Nucleotide sequence of the human parathyroid hormone gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
RN   [3]
RP   PROTEIN SEQUENCE OF 26-37.
RX   MEDLINE=74174967; PubMed=4833516;
RA   Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;
RT   "Structural analysis of human proparathyroid hormone by a new
RT   microsequencing approach.";
RL   Nature 249:155-157(1974).
RN   [4]
RP   PROTEIN SEQUENCE OF 26-40.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [5]
RP   PROTEIN SEQUENCE OF 32-68.
RX   MEDLINE=74111656; PubMed=4521809;
RA   Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
RA   O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;
RT   "The amino-acid sequence of the amino-terminal 37 residues of human
RT   parathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).
RN   [6]
RP   PROTEIN SEQUENCE OF 61-83 AND 84-115.
RX   MEDLINE=79082855; PubMed=728431;
RA   Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,
RA   Potts J.T. Jr.;
RT   "Complete amino acid sequence of human parathyroid hormone.";
RL   Biochemistry 17:5723-5729(1978).
RN   [7]
RP   PROTEIN SEQUENCE OF 75-100.
RA   Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,
RA   O'Riordan J.L.H., Potts J.T. Jr.;
RL   (In) Talmadge R.V., Owen M., Parsons J.A. (eds.);
RL   Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,
RL   Amsterdam (1975).
RN   [8]
RP   SEQUENCE REVISION.
RX   MEDLINE=75146516; PubMed=1125201;
RA   Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "A reinvestigation of the amino-terminal sequence of human parathyroid
RT   hormone.";
RL   Biochemistry 14:1842-1847(1975).
RN   [9]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=75059220; PubMed=4474131;
RA   Tregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T.,
RA   Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
RT   "Solid-phase synthesis of the biologically active N-terminal 1-34
RT   peptide of human parathyroid hormone.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
RN   [10]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=73227467; PubMed=4721748;
RA   Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
RA   Riniker B., Rittel W., Sieber P.;
RT   "Synthesis of sequence 1-34 of human parathyroid hormone.";
RL   Helv. Chim. Acta 56:470-473(1973).
RN   [11]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=91299748; PubMed=2069952;
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RA   Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
RT   "Investigation of the solution structure of the human parathyroid
RT   hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and
RT   molecular dynamics calculations.";
RL   Biochemistry 30:6936-6942(1991).
RN   [12]
RP   STRUCTURE BY NMR OF 32-65.
RX   MEDLINE=93345518; PubMed=8344299;
RA   Barden J.A., Cuthbertson R.M.;
RT   "Stabilized NMR structure of human parathyroid hormone(1-34).";
RL   Eur. J. Biochem. 215:315-321(1993).
RN   [13]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;
RA   Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
RA   Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
RA   Roesch P.;
RT   "Structure of human parathyroid hormone 1-37 in solution.";
RL   J. Biol. Chem. 270:15194-15202(1995).
RN   [14]
RP   STRUCTURE BY NMR OF 32-70.
RX   MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments hPTH(1-34)
RT   and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
RN   [15]
RP   VARIANT FIH ARG-18.
RX   MEDLINE=91009811; PubMed=2212001;
RA   Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
RA   Kronenberg H.M.;
RT   "Mutation of the signal peptide-encoding region of the
RT   preproparathyroid hormone gene in familial isolated
RT   hypoparathyroidism.";
RL   J. Clin. Invest. 86:1084-1087(1990).
RN   [16]
RP   VARIANT FIH PRO-23.
RX   PubMed=10523031;
RA   Sunthornthepvarakul T., Churesigaew S., Ngowngarmratana S.;
RT   "A novel mutation of the signal peptide of the preproparathyroid
RT   hormone gene associated with autosomal recessive familial isolated
RT   hypoparathyroidism.";
RL   J. Clin. Endocrinol. Metab. 84:3792-3796(1999).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- DISEASE: Defects in PTH are a cause of familial isolated
CC       hypoparathyroidism (FIH) [MIM:146200]. FIH exist both as autosomal
CC       dominant and recessive forms of hypoparathyroidism.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   EMBL; J00301; AAA60215.1; -; Genomic_DNA.
DR   EMBL; V00597; CAA23843.1; -; mRNA.
DR   EMBL; A29146; CAA01956.1; -; Unassigned_DNA.
DR   PIR; A19339; PTHU.
DR   PDB; 1BWX; NMR; @=32-70.
DR   PDB; 1ET1; X-ray; A/B=32-65.
DR   PDB; 1ET2; Model; A=32-65.
DR   PDB; 1FVY; NMR; A=32-62.
DR   PDB; 1HPH; NMR; @=32-68.
DR   PDB; 1HPY; NMR; @=32-65.
DR   PDB; 1HTH; NMR; @=32-65.
DR   PDB; 1ZWA; NMR; @=32-65.
DR   PDB; 1ZWB; NMR; @=33-68.
DR   PDB; 1ZWD; NMR; @=34-68.
DR   PDB; 1ZWE; NMR; @=35-68.
DR   PDB; 1ZWF; NMR; @=35-68.
DR   PDB; 1ZWG; NMR; @=-.
DR   Ensembl; ENSG00000152266; Homo sapiens.
DR   HGNC; HGNC:9606; PTH.
DR   MIM; 168450; -.
DR   MIM; 146200; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   GO; GO:0045453; P:bone resorption; NAS.
DR   GO; GO:0006874; P:calcium ion homeostasis; NAS.
DR   GO; GO:0046058; P:cAMP metabolism; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
DR   GO; GO:0001501; P:skeletal development; TAS.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   3D-structure; Direct protein sequencing; Disease mutation; Hormone;
KW   Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
FT   VARIANT      18     18       C -> R (in FIH; dominant; leads to
FT                                inefficient processing of the precursor).
FT                                /FTId=VAR_006047.
FT   VARIANT      23     23       S -> P (in FIH; recessive, might lead to
FT                                inefficient processing of the precursor).
FT                                /FTId=VAR_018464.
FT   CONFLICT    107    107       N -> D (in Ref. 6).
FT   HELIX        34     64
SQ   SEQUENCE   115 AA;  12861 MW;  849015736A6E5597 CRC64;

  Query Match             67.5%;  Score 56;  DB 1;  Length 115;
  Best Local Similarity   91.7%;  Pred. No. 0.67;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :||||||||||||
Db         32 SVSEIQLMHNLG 43


RESULT 8
PTHY_MACFA
ID   PTHY_MACFA     STANDARD;      PRT;   115 AA.
AC   Q9XT35;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Malaivijitnond S., Takenaka O.;
RT   "Nucleotide sequences of parathyroid gene in five species of macaque
RT   of Thailand.";
RL   J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------------
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AF130257; AAD42777.1; -; Genomic_DNA.
DR   HSSP; P01270; 1ET1.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       By similarity.
FT   PROPEP       26     31       By similarity.
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12890 MW;  8C2500EF24BE5597 CRC64;

  Query Match             67.5%;  Score 56;  DB 1;  Length 115;
  Best Local Similarity   91.7%;  Pred. No. 0.67;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :|||||||||||
Db         32 SVSEIQLMHNLG 43


RESULT 9
PTHY_PIG
ID   PTHY_PIG       STANDARD;      PRT;   115 AA.
AC   P01269;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87316938; PubMed=3628009;
RA   Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT   "Nucleotide sequence of a full-length cDNA clone encoding
RT   preproparathyroid hormone from pig and rat.";
RL   Nucleic Acids Res. 15:6740-6740(1987).
RN   [2]
RP   PROTEIN SEQUENCE OF 26-115.
RX   MEDLINE=76018954; PubMed=1164500;
RA   Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
RT   "Porcine proparathyroid hormone. Identification, biosynthesis, and
RT   partial amino acid sequence.";
RL   Biochemistry 14:3631-3635(1975).
RN   [3]
RP   PROTEIN SEQUENCE OF 32-115.
RX   MEDLINE=74253317; PubMed=4840833;
RA   Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA   Potts J.T. Jr.;
RT   "The amino acid sequence of porcine parathyroid hormone.";
RL   Biochemistry 13:1994-1999(1974).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; X05722; CAA29193.1; -; mRNA.
DR   PIR; B26806; PTPG.
DR   HSSP; P01270; 1BWX.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Direct protein sequencing; Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12852 MW;  9FE8BCDE614BAC16 CRC64;

  Query Match             67.5%;  Score 56;  DB 1;  Length 115;
  Best Local Similarity   91.7%;  Pred. No. 0.67;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :|||||||||||
Db         32 SVSEIQLMHNLG 43


RESULT 10
Q4VB48_HUMAN
ID   Q4VB48_HUMAN PRELIMINARY;      PRT;   115 AA.
AC   Q4VB48;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Parathyroid hormone, preproprotein.
GN   Name=PTH;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC096143; AAH96143.1; -; mRNA.
DR   EMBL; BC096144; AAH96144.1; -; mRNA.
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DR   EMBL; BC096145; AAH96145.1; -; mRNA.
DR   EMBL; BC096142; AAH96142.1; -; mRNA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
SQ   SEQUENCE   115 AA;  12861 MW;  849015736A6E5597 CRC64;

  Query Match             67.5%;  Score 56;  DB 2;  Length 115;
  Best Local Similarity   91.7%;  Pred. No. 0.67;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :|||||||||||
Db         32 SVSEIQLMHNLG 43


RESULT 11
Q5TLZ1_BRARE
ID   Q5TLZ1_BRARE PRELIMINARY;      PRT;   102 AA.
AC   Q5TLZ1;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Parathyroid hormone.
GN   Name=pth1; Synonyms=PTH;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Okabe M., Graham A.;
RT   "The origin of the parathyroid gland.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:17716-17719(2004).
DR   EMBL; AB175679; BAD72832.1; -; mRNA.
DR   ZFIN; ZDB-GENE-040623-1; pth1.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
SQ   SEQUENCE   102 AA;  11641 MW;  5AA7B0F8A4110764 CRC64;

  Query Match             66.3%;  Score 55;  DB 2;  Length 102;
  Best Local Similarity   83.3%;  Pred. No. 0.84;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||:|:|||||||
Db         36 AVNEVQLMHNLG 47


RESULT 12
Q6WQ25_BRARE
ID   Q6WQ25_BRARE PRELIMINARY;      PRT;   102 AA.
AC   Q6WQ25;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Parathyroid hormone ligand type-1.
GN   Name=pth1;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14684608; DOI=10.1210/en.2003-0964;
RA   Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
RA   Bastepe M., Rubin D.A., Juppner H.;
RT   "Identification and characterization of two parathyroid hormone-like
RT   molecules in zebrafish.";
RL   Endocrinology 145:1634-1639(2004).
DR   EMBL; AY275669; AAQ16566.1; -; mRNA.
DR   ZFIN; ZDB-GENE-040623-1; pth1.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
SQ   SEQUENCE   102 AA;  11690 MW;  5AA7A84FF4110764 CRC64;

  Query Match             66.3%;  Score 55;  DB 2;  Length 102;
  Best Local Similarity   83.3%;  Pred. No. 0.84;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||:|:|||||||
Db         36 AVNEVQLMHNLG 47


RESULT 13
PTHY_BOVIN
ID   PTHY_BOVIN     STANDARD;      PRT;   115 AA.
AC   P01268;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=80056617; PubMed=388425;
RA   Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA   Potts J.T. Jr., Rich A.;
RT   "Cloning and nucleotide sequence of DNA coding for bovine
RT   preproparathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82037785; PubMed=6170060;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Introduction by molecular cloning of artifactual inverted sequences
RT   at the 5' terminus of the sense strand of bovine parathyroid hormone
RT   cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8;
RA   Weaver C.A., Gordon D.F., Kemper B.;
RT   "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL   Mol. Cell. Endocrinol. 28:411-424(1982).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84262483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
RA   Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT   "Isolation and complete nucleotide sequence of the gene for bovine
RT   parathyroid hormone.";
RL   Gene 28:319-329(1984).
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RN   [5]
RP   PROTEIN SEQUENCE OF 26-115.
RX   MEDLINE=74142666; PubMed=4522780;
RA   Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA   Cohn D.V.;
RT   "The N-terminal amino-acid sequence of bovine proparathyroid
RT   hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN   [6]
RP   PROTEIN SEQUENCE OF 32-115.
RX   MEDLINE=71076162; PubMed=5531031;
RA   Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
RA   Aurbach G.D., Potts J.T. Jr.;
RT   "The amino acid sequence of bovine parathyroid hormone I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN   [7]
RP   PROTEIN SEQUENCE OF 32-115.
RX   MEDLINE=71063634; PubMed=5275384;
RA   Brewer H.B. Jr., Ronan R.;
RT   "Bovine parathyroid hormone: amino acid sequence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN   [8]
RP   SYNTHESIS OF 32-65.
RX   MEDLINE=71091588; PubMed=4322265;
RA   Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA   Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT   "Synthesis of a biologically active N-terminal tetratriacontapeptide
RT   of parathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN   [9]
RP   STRUCTURE BY NMR OF 32-68.
RX   MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
RA   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT   "Solution structures of human parathyroid hormone fragments hPTH(1-34)
RT   and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
RL   Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; V00106; CAA23439.1; -; mRNA.
DR   EMBL; J00024; AAA30747.1; -; mRNA.
DR   EMBL; K01938; AAA30749.1; -; Genomic_DNA.
DR   EMBL; M25082; AAA30748.1; -; mRNA.
DR   PIR; A24949; PTBO.
DR   PDB; 1ZWC; NMR; @=32-68.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   3D-structure; Direct protein sequencing; Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    115       Parathyroid hormone.
FT   CONFLICT    106    106       V -> G (in Ref. 4).
FT   HELIX         37     40
FT   TURN          41     42
FT   TURN          51     52
FT   HELIX         53     60
FT   TURN          61     63
SQ   SEQUENCE   115 AA;  12980 MW;  2ED246B348880710 CRC64;

  Query Match             66.3%;  Score 55;  DB 1;  Length 115;
  Best Local Similarity   91.7%;  Pred. No. 0.96;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              |||||| |||||
Db         32 AVSEIQFMHNLG 43


RESULT 14
PTHY_CHICK
ID   PTHY_CHICK     STANDARD;      PRT;   119 AA.
AC   P15743;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Parathyroid hormone precursor (PTH).
GN   Name=PTH;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89219100; PubMed=2710135;
RA   Russell J., Sherwood L.M.;
RT   "Nucleotide sequence of the DNA complementary to avian (chicken)
RT   preproparathyroid hormone mRNA and the deduced sequence of the hormone
RT   precursor.";
RL   Mol. Endocrinol. 3:325-331(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89284968; PubMed=3251402;
RA   Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
RA   Kronenberg H.M.;
RT   "Nucleotide sequence of cloned cDNAs encoding chicken
RT   preproparathyroid hormone.";
RL   J. Bone Miner. Res. 3:689-698(1988).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M31604; AAA49093.1; -; mRNA.
DR   EMBL; M36522; AAB02866.1; -; mRNA.
DR   PIR; A34937; A34937.
DR   HSSP; P01270; 1FVY.
DR   Ensembl; ENSGALG00000005358; Gallus gallus.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003626; PTH_related.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD013225; PTH_related; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25
FT   PROPEP       26     31
FT   CHAIN        32    119       Parathyroid hormone.
SQ   SEQUENCE   119 AA;  13943 MW;  B309D8E772997F6E CRC64;

  Query Match             63.9%;  Score 53;  DB 1;  Length 119;
  Best Local Similarity   83.3%;  Pred. No. 2.1;
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  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :|||:|||||||
Db         32 SVSEMQLMHNLG 43


RESULT 15
PTHY_CANFA
ID   PTHY_CANFA     STANDARD;      PRT;   115 AA.
AC   P52212;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Parathyroid;
RX   MEDLINE=95369696; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;
RA   Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W.,
RA   Capen C.C.;
RT   "Sequences of the cDNAs encoding canine parathyroid hormone-related
RT   protein and parathyroid hormone.";
RL   Gene 160:241-243(1995).
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U15662; AAA82584.1; -; mRNA.
DR   PIR; JC4202; JC4202.
DR   HSSP; P01268; 1ZWC.
DR   Ensembl; ENSCAFG00000008177; Canis familiaris.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       By similarity.
FT   PROPEP       26     31       By similarity.
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12957 MW;  FC38F77F1C8CFE56 CRC64;

  Query Match             62.7%;  Score 52;  DB 1;  Length 115;
  Best Local Similarity   83.3%;  Pred. No. 2.8;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :||||| |||||
Db         32 SVSEIQFMHNLG 43


RESULT 16
PTHY_FELCA
ID   PTHY_FELCA     STANDARD;      PRT;   115 AA.
AC   Q9GL67;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Parathyroid hormone precursor (Parathyrin) (PTH).
GN   Name=PTH;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT   "Molecular cloning of feline preproparathyroid hormone.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC       bone and preventing their renal excretion (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF309967; AAG30545.1; -; mRNA.
DR   HSSP; P01268; 1ZWC.
DR   InterPro; IPR001415; Parathyrd_hrm.
DR   InterPro; IPR003625; Pthyrhorm_sub.
DR   PANTHER; PTHR10541; Pthyrhorm_sub; 1.
DR   Pfam; PF01279; Parathyroid; 1.
DR   PIRSF; PIRSF001832; PTH; 1.
DR   ProDom; PD010687; Pthyrhorm_sub; 1.
DR   SMART; SM00087; PTH; 1.
DR   PROSITE; PS00335; PARATHYROID; 1.
KW   Hormone; Signal.
FT   SIGNAL        1     25       By similarity.
FT   PROPEP       26     31       By similarity.
FT   CHAIN        32    115       Parathyroid hormone.
SQ   SEQUENCE   115 AA;  12921 MW;  80CD557CC6A1A47E CRC64;

  Query Match             62.7%;  Score 52;  DB 1;  Length 115;
  Best Local Similarity   83.3%;  Pred. No. 2.8;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :||||| |||||
Db         32 SVSEIQFMHNLG 43


RESULT 17
Q8TVL1_METKA
ID   Q8TVL1_METKA PRELIMINARY;      PRT;   394 AA.
AC   Q8TVL1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Acetyl-CoA acetyltransferase.
GN   OrderedLocusNames=MK1378;
OS   Methanopyrus kandleri.
OC   Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC   Methanopyrus.
OX   NCBI_TaxID=2320;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=AV19 / DSM 6324 / JCM 9639;
RX   MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RA   Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA   Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA   Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA   Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT   "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT   and monophyly of archaeal methanogens.";
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RL   Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR   EMBL; AE010431; AAM02591.1; -; Genomic_DNA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR002155; Thiolase.
DR   Pfam; PF02803; Thiolase_C; 1.
DR   Pfam; PF00108; Thiolase_N; 1.
KW   Complete proteome; Transferase.
SQ   SEQUENCE   394 AA;  42063 MW;  A816CFFFFDE634E4 CRC64;

  Query Match             60.2%;  Score 50;  DB 2;  Length 394;
  Best Local Similarity   64.3%;  Pred. No. 23;
  Matches    9;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 SEIQLMHNLGGGGG 16
              :|| | ||:|| ||
Db        370 AEIGLTHNVGGSGG 383


RESULT 18
Q55GS9_DICDI
ID   Q55GS9_DICDI PRELIMINARY;      PRT;   885 AA.
AC   Q55GS9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=DDB0189350;
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AX4;
RA   Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA   Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA   Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA   Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA   Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA   Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA   Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA   Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA   Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA   Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA   Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA   Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA   Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
RA   Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA   Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA   Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA   Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA   Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT   "The genome of the social amoeba Dictyostelium discoideum.";
RL   Nature 0:0-0(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAFI01000009; EAL73219.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   885 AA;  97636 MW;  7F56E9DFBC85BEEA CRC64;

  Query Match             59.0%;  Score 49;  DB 2;  Length 885;
  Best Local Similarity   55.0%;  Pred. No. 84;
  Matches   11;  Conservative    2;  Mismatches    1;  Indels    6;  Gaps    1;

Qy          3 SEIQLMH------NLGGGGG 16
              | |||:|      |:|||||
Db        157 SPIQLIHPNLDSPNVGGGGG 176


RESULT 19
Q5SXZ6_MOUSE
ID   Q5SXZ6_MOUSE PRELIMINARY;      PRT;   140 AA.
AC   Q5SXZ6;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Novel protein (Fragment).
GN   Name=OTTMUSP00000001188; ORFNames=RP23-50E4.2-005;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Phillimore B.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL592065; CAI25864.1; -; Genomic_DNA.
FT   NON_TER     140    140
SQ   SEQUENCE   140 AA;  15387 MW;  F5108D76C2FFD8EE CRC64;

  Query Match             57.8%;  Score 48;  DB 2;  Length 140;
  Best Local Similarity   62.5%;  Pred. No. 15;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGGGG 16
              |  | || | |||| |
Db         92 ASKEQQLRHKLGGGSG 107


RESULT 20
Q5SXZ5_MOUSE
ID   Q5SXZ5_MOUSE PRELIMINARY;      PRT;   190 AA.
AC   Q5SXZ5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Novel protein (Fragment).
GN   Name=OTTMUSP00000001189; ORFNames=RP23-50E4.2-007;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Phillimore B.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL592065; CAI25865.1; -; Genomic_DNA.
FT   NON_TER     190    190
SQ   SEQUENCE   190 AA;  20892 MW;  F0DC4B41A26B53C5 CRC64;

  Query Match             57.8%;  Score 48;  DB 2;  Length 190;
  Best Local Similarity   62.5%;  Pred. No. 21;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGGGG 16
              |  | || | |||| |
Db         92 ASKEQQLRHKLGGGSG 107


Search completed: November 21, 2005, 16:42:55
Job time : 238 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:38:20 ; Search time 46 Seconds
(without alignments)
28.757 Million cell updates/sec

Title: SEQ-NEW
Perfect score: 83
Sequence: 1 avseiqlmhnlggggg 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59	71.1	12	2	US-09-730-174A-5	Sequence 5, Appli
2	59	71.1	14	2	US-09-421-379-5	Sequence 5, Appli
3	59	71.1	15	2	US-09-730-174A-11	Sequence 11, Appl
4	59	71.1	27	2	US-09-448-867-5	Sequence 5, Appli
5	59	71.1	27	2	US-09-448-867-9	Sequence 9, Appli
6	59	71.1	27	2	US-09-447-800-7	Sequence 7, Appli
7	59	71.1	27	2	US-10-157-076-5	Sequence 5, Appli
8	59	71.1	27	2	US-10-157-076-9	Sequence 9, Appli
9	59	71.1	28	2	US-09-448-867-4	Sequence 4, Appli
10	59	71.1	28	2	US-09-448-867-8	Sequence 8, Appli
11	59	71.1	28	2	US-10-157-076-4	Sequence 4, Appli
12	59	71.1	28	2	US-10-157-076-8	Sequence 8, Appli
13	59	71.1	30	2	US-09-843-221A-48	Sequence 48, Appl
14	59	71.1	31	2	US-09-228-990-31	Sequence 31, Appl
15	59	71.1	33	2	US-09-447-800-6	Sequence 6, Appli
16	59	71.1	34	1	US-08-488-105-3	Sequence 3, Appli
17	59	71.1	34	1	US-08-488-105-9	Sequence 9, Appli
18	59	71.1	34	1	US-08-488-105-15	Sequence 15, Appl
19	59	71.1	34	2	US-09-447-800-5	Sequence 5, Appli
20	59	71.1	34	2	US-09-843-221A-25	Sequence 25, Appl
21	59	71.1	34	2	US-09-623-548A-274	Sequence 274, App
22	59	71.1	34	2	US-10-340-484-22	Sequence 22, Appl
23	59	71.1	34	2	US-10-340-484-23	Sequence 23, Appl
24	59	71.1	34	2	US-09-657-276-274	Sequence 274, App
25	59	71.1	35	1	US-08-142-551B-52	Sequence 52, Appl
26	59	71.1	84	2	US-09-843-221A-11	Sequence 11, Appl
27	57	68.7	31	2	US-09-228-990-32	Sequence 32, Appl
28	57	68.7	35	1	US-08-142-551B-56	Sequence 56, Appl
29	56	67.5	12	2	US-09-730-174A-3	Sequence 3, Appli
30	56	67.5	13	1	US-08-411-726-3	Sequence 3, Appli
31	56	67.5	14	2	US-09-421-379-3	Sequence 3, Appli
32	56	67.5	15	2	US-09-730-174A-9	Sequence 9, Appli
33	56	67.5	27	2	US-09-448-867-7	Sequence 7, Appli
34	56	67.5	27	2	US-09-448-867-13	Sequence 13, Appl
35	56	67.5	27	2	US-09-447-800-10	Sequence 10, Appl
36	56	67.5	27	2	US-10-157-076-7	Sequence 7, Appli
37	56	67.5	27	2	US-10-157-076-13	Sequence 13, Appl
38	56	67.5	28	2	US-09-406-813-3	Sequence 3, Appli
39	56	67.5	28	2	US-09-406-813-6	Sequence 6, Appli
40	56	67.5	28	2	US-09-448-867-6	Sequence 6, Appli
41	56	67.5	28	2	US-09-448-867-12	Sequence 12, Appl
42	56	67.5	28	2	US-09-843-221A-52	Sequence 52, Appl
43	56	67.5	28	2	US-09-843-221A-168	Sequence 168, App
44	56	67.5	28	2	US-10-157-076-6	Sequence 6, Appli
45	56	67.5	28	2	US-10-157-076-12	Sequence 12, Appl
46	56	67.5	29	2	US-09-406-813-4	Sequence 4, Appli
47	56	67.5	29	2	US-09-843-221A-51	Sequence 51, Appl
48	56	67.5	29	2	US-09-843-221A-167	Sequence 167, App
49	56	67.5	30	1	US-08-262-495C-5	Sequence 5, Appli
50	56	67.5	30	1	US-08-262-495C-6	Sequence 6, Appli
51	56	67.5	30	2	US-08-904-760B-7	Sequence 7, Appli
52	56	67.5	30	2	US-08-904-760B-33	Sequence 33, Appl
53	56	67.5	30	2	US-08-904-760B-34	Sequence 34, Appl
54	56	67.5	30	2	US-08-904-760B-35	Sequence 35, Appl
55	56	67.5	30	2	US-09-536-785A-7	Sequence 7, Appli
56	56	67.5	30	2	US-09-536-785A-33	Sequence 33, Appl
57	56	67.5	30	2	US-09-536-785A-34	Sequence 34, Appl
58	56	67.5	30	2	US-09-536-785A-35	Sequence 35, Appl
59	56	67.5	30	2	US-09-843-221A-39	Sequence 39, Appl
60	56	67.5	30	2	US-09-843-221A-42	Sequence 42, Appl
61	56	67.5	30	2	US-09-843-221A-47	Sequence 47, Appl
62	56	67.5	30	2	US-09-843-221A-49	Sequence 49, Appl
63	56	67.5	30	2	US-09-843-221A-50	Sequence 50, Appl
64	56	67.5	30	2	US-09-843-221A-124	Sequence 124, App
65	56	67.5	30	2	US-09-843-221A-125	Sequence 125, App
66	56	67.5	30	2	US-09-843-221A-126	Sequence 126, App
67	56	67.5	30	2	US-09-843-221A-127	Sequence 127, App
68	56	67.5	30	2	US-09-843-221A-166	Sequence 166, App
69	56	67.5	31	1	US-08-262-495C-3	Sequence 3, Appli
70	56	67.5	31	1	US-08-262-495C-4	Sequence 4, Appli
71	56	67.5	31	1	US-08-691-647C-1	Sequence 1, Appli
72	56	67.5	31	1	US-08-691-647C-2	Sequence 2, Appli
73	56	67.5	31	1	US-08-691-647C-3	Sequence 3, Appli
74	56	67.5	31	1	US-08-691-647C-4	Sequence 4, Appli
75	56	67.5	31	1	US-08-691-647C-6	Sequence 6, Appli
76	56	67.5	31	2	US-08-904-760B-1	Sequence 1, Appli
77	56	67.5	31	2	US-08-904-760B-2	Sequence 2, Appli
78	56	67.5	31	2	US-08-904-760B-3	Sequence 3, Appli
79	56	67.5	31	2	US-08-904-760B-4	Sequence 4, Appli
80	56	67.5	31	2	US-08-904-760B-5	Sequence 5, Appli
81	56	67.5	31	2	US-08-904-760B-6	Sequence 6, Appli
82	56	67.5	31	2	US-08-904-760B-8	Sequence 8, Appli
83	56	67.5	31	2	US-08-904-760B-11	Sequence 11, Appl
84	56	67.5	31	2	US-08-904-760B-12	Sequence 12, Appl
85	56	67.5	31	2	US-08-904-760B-14	Sequence 14, Appl
86	56	67.5	31	2	US-08-904-760B-15	Sequence 15, Appl
87	56	67.5	31	2	US-08-904-760B-16	Sequence 16, Appl
88	56	67.5	31	2	US-08-904-760B-17	Sequence 17, Appl
89	56	67.5	31	2	US-08-904-760B-18	Sequence 18, Appl
90	56	67.5	31	2	US-08-904-760B-19	Sequence 19, Appl
91	56	67.5	31	2	US-08-904-760B-20	Sequence 20, Appl
92	56	67.5	31	2	US-08-904-760B-21	Sequence 21, Appl
93	56	67.5	31	2	US-08-904-760B-32	Sequence 32, Appl
94	56	67.5	31	2	US-09-406-813-2	Sequence 2, Appli
95	56	67.5	31	2	US-09-406-813-5	Sequence 5, Appli
96	56	67.5	31	2	US-09-536-785A-1	Sequence 1, Appli
97	56	67.5	31	2	US-09-536-785A-2	Sequence 2, Appli
98	56	67.5	31	2	US-09-536-785A-3	Sequence 3, Appli
99	56	67.5	31	2	US-09-536-785A-4	Sequence 4, Appli
100	56	67.5	31	2	US-09-536-785A-5	Sequence 5, Appli

ALIGNMENTS

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RESULT 1
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. 6838264
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

  Query Match             71.1%;  Score 59;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.0088;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 2
US-09-421-379-5
; Sequence 5, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-5

  Query Match             71.1%;  Score 59;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 3
US-09-730-174A-11
; Sequence 11, Application US/09730174A
; Patent No. 6838264
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 11
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-11

  Query Match             71.1%;  Score 59;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 4
US-09-448-867-5
; Sequence 5, Application US/09448867
; Patent No. 6417333
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J
;  APPLICANT: POTTS JR., JOHN T.
;  TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION
;  TITLE OF INVENTION: AND USE
;  FILE REFERENCE: 0609.4640001
;  CURRENT APPLICATION NUMBER: US/09/448,867
;  CURRENT FILING DATE: 1999-11-24
;  EARLIER APPLICATION NUMBER: 60/109,938
;  EARLIER FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-448-867-5

  Query Match             71.1%;  Score 59;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 5
US-09-448-867-9
; Sequence 9, Application US/09448867
; Patent No. 6417333
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J
;  APPLICANT: POTTS JR., JOHN T.
;  TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION
;  TITLE OF INVENTION: AND USE
;  FILE REFERENCE: 0609.4640001
;  CURRENT APPLICATION NUMBER: US/09/448,867
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;  CURRENT FILING DATE: 1999-11-24
;  EARLIER APPLICATION NUMBER: 60/109,938
;  EARLIER FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-448-867-9

  Query Match             71.1%;  Score 59;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 6
US-09-447-800-7
; Sequence 7, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION: ANALOGS
;  FILE REFERENCE: 0609.4630001
;  CURRENT APPLICATION NUMBER: US/09/447,800
;  CURRENT FILING DATE: 1999-11-23
;  EARLIER APPLICATION NUMBER: 60/110,152
;  EARLIER FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-09-447-800-7

  Query Match             71.1%;  Score 59;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 7
US-10-157-076-5
; Sequence 5, Application US/10157076
; Patent No. 6803213
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/157,076
;  CURRENT FILING DATE:  2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-157-076-5

  Query Match             71.1%;  Score 59;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 8
US-10-157-076-9
; Sequence 9, Application US/10157076
; Patent No. 6803213
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/157,076
;  CURRENT FILING DATE:  2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-157-076-9

  Query Match             71.1%;  Score 59;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 9
US-09-448-867-4
; Sequence 4, Application US/09448867
; Patent No. 6417333
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J
;  APPLICANT: POTTS JR., JOHN T.
;  TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION
;  TITLE OF INVENTION: AND USE
;  FILE REFERENCE: 0609.4640001
;  CURRENT APPLICATION NUMBER: US/09/448,867
;  CURRENT FILING DATE: 1999-11-24
;  EARLIER APPLICATION NUMBER: 60/109,938
;  EARLIER FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-09-448-867-4

  Query Match 71.1%; Score 59; DB 2; Length 28;
  Best Local Similarity 100.0%; Pred. No. 0.021;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

RESULT 10
US-09-448-867-8
; Sequence 8, Application US/09448867
; Patent No. 6417333
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J
; APPLICANT: POTTS JR., JOHN T.
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 0609.4640001
; CURRENT APPLICATION NUMBER: US/09/448,867
; CURRENT FILING DATE: 1999-11-24
; EARLIER APPLICATION NUMBER: 60/109,938
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-448-867-8

  Query Match 71.1%; Score 59; DB 2; Length 28;
  Best Local Similarity 100.0%; Pred. No. 0.021;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

RESULT 11
US-10-157-076-4
; Sequence 4, Application US/10157076
; Patent No. 6803213
; GENERAL INFORMATION:
; APPLICANT: Bringhurst, F. Richard
; APPLICANT: Takasu, Hisashi
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Potts, John T. Jr.
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
; FILE REFERENCE: 0609.4640002
; CURRENT APPLICATION NUMBER: US/10/157,076
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 09/448,867
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 60/109,938
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-076-4

  Query Match 71.1%; Score 59; DB 2; Length 28;
  Best Local Similarity 100.0%; Pred. No. 0.021;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

RESULT 12
US-10-157-076-8
; Sequence 8, Application US/10157076
; Patent No. 6803213
; GENERAL INFORMATION:
; APPLICANT: Bringhurst, F. Richard
; APPLICANT: Takasu, Hisashi
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Potts, John T. Jr.
; TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
; FILE REFERENCE: 0609.4640002
; CURRENT APPLICATION NUMBER: US/10/157,076
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 09/448,867
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US 60/109,938
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-076-8

  Query Match 71.1%; Score 59; DB 2; Length 28;
  Best Local Similarity 100.0%; Pred. No. 0.021;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
Db 1 AVSEIQLMHNLG 12

RESULT 13
US-09-843-221A-48
; Sequence 48, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HC
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat PTH
US-09-843-221A-48

  Query Match 71.1%; Score 59; DB 2; Length 30;
  Best Local Similarity 100.0%; Pred. No. 0.023;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12

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Db          1 AVSEIQLMHNLG 12


RESULT 14
US-09-228-990-31
; Sequence 31, Application US/09228990
; Patent No. 6472505
;  GENERAL INFORMATION:
;    APPLICANT:  Condon, Stephen M.
;    APPLICANT:  Morize, Isabelle
;    TITLE OF INVENTION:  PEPTIDE PARATHYROID HORMONE ANALOGS
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, Mailstop 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/228,990
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/046,472
;      FILING DATE:  14-MAY-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Martin Esq., Michael B.
;      REGISTRATION NUMBER:  37,521
;      REFERENCE/DOCKET NUMBER:  A2678B-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-2793
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  N-terminal
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  8
;      OTHER INFORMATION:  /product= "Nle"
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  18..22
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "The side chains of Lys at position 18 and Asp at
;      OTHER INFORMATION:  position 22 are linked by an amide bond. "
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  31
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "This C-terminal amino acid is an amide, i.e., CONH2."
US-09-228-990-31

  Query Match             71.1%;  Score 59;  DB 2;  Length 31;
  Best Local Similarity   92.3%;  Pred. No. 0.023;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGG 13
              ||||||| |||||
Db          1 AVSEIQLXHNLGG 13


RESULT 15
US-09-447-800-6
; Sequence 6, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION: ANALOGS
;  FILE REFERENCE: 0609.4630001
;  CURRENT APPLICATION NUMBER: US/09/447,800
;  CURRENT FILING DATE: 1999-11-23
;  EARLIER APPLICATION NUMBER: 60/110,152
;  EARLIER FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-09-447-800-6

  Query Match             71.1%;  Score 59;  DB 2;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
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Db          1 AVSEIQLMHNLG 12


RESULT 16
US-08-488-105-3
; Sequence 3, Application US/08488105
; Patent No. 5717062
;  GENERAL INFORMATION:
;    APPLICANT:  Chorev, Michael
;    APPLICANT:  Rosenblatt, Michael
;    TITLE OF INVENTION:  CYCLIC ANALOGS OF PTH AND PTHrP
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,105
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tsao, Y. Rocky
;      REGISTRATION NUMBER:  34,053
;      REFERENCE/DOCKET NUMBER:  00537/112001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
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;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       OTHER INFORMATION:  The side chains of Lys at
;       OTHER INFORMATION:  position 13 and Asp at postion 17 are linked by an amide bond
;       OTHER INFORMATION:  and this sequence has an amide C-terminus (i.e., CONH2), rath
;       OTHER INFORMATION:  than a carboxy C-terminus (i.e., COOH).
US-08-488-105-3

  Query Match             71.1%;  Score 59;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.026;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
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Db          1 AVSEIQLMHNLG 12


RESULT 17
US-08-488-105-9
; Sequence 9, Application US/08488105
; Patent No. 5717062
;  GENERAL INFORMATION:
;    APPLICANT:  Chorev, Michael
;    APPLICANT:  Rosenblatt, Michael
;    TITLE OF INVENTION:  CYCLIC ANALOGS OF PTH AND PTHrP
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,105
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tsao, Y. Rocky
;      REGISTRATION NUMBER:  34,053
;      REFERENCE/DOCKET NUMBER:  00537/112001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      OTHER INFORMATION:  The side chains of Lys at
;      OTHER INFORMATION:  position 26 and Asp at position 30 are linked by an amide bon
;      OTHER INFORMATION:  and this sequence has an amide C-terminus (i.e., CONH2), rath
;      OTHER INFORMATION:  than a carboxy C-terminus (i.e., COOH).
US-08-488-105-9

  Query Match             71.1%;  Score 59;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.026;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 18
US-08-488-105-15
; Sequence 15, Application US/08488105
; Patent No. 5717062
;  GENERAL INFORMATION:
;    APPLICANT:  Chorev, Michael
;    APPLICANT:  Rosenblatt, Michael
;    TITLE OF INVENTION:  CYCLIC ANALOGS OF PTH AND PTHrP
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,105
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tsao, Y. Rocky
;      REGISTRATION NUMBER:  34,053
;      REFERENCE/DOCKET NUMBER:  00537/112001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      OTHER INFORMATION:  The side chains of Lys at
;      OTHER INFORMATION:  position 13 and Asp at position 17 and the side chains of Lys
;      OTHER INFORMATION:  position 26 and Asp at position 30 are linked byy an amide bor
;      OTHER INFORMATION:  and this sequence has an amide C-terminus (i.e., COOH).
US-08-488-105-15

  Query Match             71.1%;  Score 59;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.026;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 19
US-09-447-800-5
; Sequence 5, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT: TAKASU, HISASHI
;  APPLICANT: GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION: ANALOGS
;  FILE REFERENCE: 0609.4630001
;  CURRENT APPLICATION NUMBER: US/09/447,800
;  CURRENT FILING DATE: 1999-11-23
;  EARLIER APPLICATION NUMBER: 60/110,152
;  EARLIER FILING DATE: 1998-11-25
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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-09-447-800-5

Query Match 71.1%; Score 59; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
||||||||||||
Db 1 AVSEIQLMHNLG 12

RESULT 20
US-09-843-221A-25
; Sequence 25, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-843-221A-25

Query Match 71.1%; Score 59; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
||||||||||||
Db 1 AVSEIQLMHNLG 12

Search completed: November 21, 2005, 16:53:33
Job time : 47 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:39:00 ; Search time 163 Seconds
(without alignments)
41.014 Million cell updates/sec

Title: SEQ-NEW
Perfect score: 83
Sequence: 1 avseiqlmhnlggggg 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_Main:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59	71.1	12	3	US-09-730-174A-5	Sequence 5, Appli
2	59	71.1	12	5	US-10-998-927-5	Sequence 5, Appli
3	59	71.1	13	3	US-09-898-398-3	Sequence 3, Appli
4	59	71.1	13	5	US-10-921-368-3	Sequence 3, Appli
5	59	71.1	14	4	US-10-192-673-5	Sequence 5, Appli
6	59	71.1	15	3	US-09-730-174A-11	Sequence 11, Appl
7	59	71.1	15	5	US-10-998-927-11	Sequence 11, Appl
8	59	71.1	21	5	US-10-484-080-18	Sequence 18, Appl
9	59	71.1	27	4	US-10-361-928-7	Sequence 7, Appli
10	59	71.1	27	4	US-10-157-076-5	Sequence 5, Appli
11	59	71.1	27	4	US-10-157-076-9	Sequence 9, Appli
12	59	71.1	27	5	US-10-959-605-5	Sequence 5, Appli
13	59	71.1	27	5	US-10-959-605-9	Sequence 9, Appli
14	59	71.1	28	4	US-10-157-076-4	Sequence 4, Appli
15	59	71.1	28	4	US-10-157-076-8	Sequence 8, Appli
16	59	71.1	28	5	US-10-959-605-4	Sequence 4, Appli
17	59	71.1	28	5	US-10-959-605-8	Sequence 8, Appli
18	59	71.1	30	3	US-09-843-221A-48	Sequence 48, Appl
19	59	71.1	30	3	US-09-999-608-48	Sequence 48, Appl
20	59	71.1	30	4	US-10-839-037-48	Sequence 48, Appl
21	59	71.1	31	4	US-10-097-079-31	Sequence 31, Appl
22	59	71.1	33	4	US-10-361-928-6	Sequence 6, Appli
23	59	71.1	34	3	US-09-843-221A-25	Sequence 25, Appl
24	59	71.1	34	3	US-09-999-608-25	Sequence 25, Appl
25	59	71.1	34	4	US-10-361-928-5	Sequence 5, Appli
26	59	71.1	34	4	US-10-340-484-22	Sequence 22, Appl
27	59	71.1	34	4	US-10-340-484-23	Sequence 23, Appl
28	59	71.1	34	4	US-10-839-037-25	Sequence 25, Appl
29	59	71.1	34	5	US-10-428-377-46	Sequence 46, Appl
30	59	71.1	34	5	US-10-484-080-30	Sequence 30, Appl
31	59	71.1	34	5	US-10-638-265-87	Sequence 87, Appl
32	59	71.1	34	6	US-11-066-697-274	Sequence 274, App
33	59	71.1	84	3	US-09-843-221A-11	Sequence 11, Appl
34	59	71.1	84	3	US-09-999-608-11	Sequence 11, Appl
35	59	71.1	84	4	US-10-215-770-5	Sequence 5, Appli
36	59	71.1	84	4	US-10-398-449-16	Sequence 16, Appl
37	59	71.1	84	4	US-10-311-366-11	Sequence 11, Appl
38	59	71.1	84	4	US-10-839-037-11	Sequence 11, Appl
39	59	71.1	84	5	US-10-617-489-2	Sequence 2, Appli
40	59	71.1	84	5	US-10-617-489-3	Sequence 3, Appli
41	59	71.1	84	5	US-10-638-265-86	Sequence 86, Appl
42	57	68.7	31	4	US-10-097-079-32	Sequence 32, Appl
43	56	67.5	12	3	US-09-730-174A-3	Sequence 3, Appli
44	56	67.5	12	5	US-10-998-927-3	Sequence 3, Appli
45	56	67.5	13	3	US-09-898-398-4	Sequence 4, Appli
46	56	67.5	13	5	US-10-921-368-4	Sequence 4, Appli
47	56	67.5	14	4	US-10-192-673-3	Sequence 3, Appli
48	56	67.5	15	3	US-09-730-174A-9	Sequence 9, Appli
49	56	67.5	15	5	US-10-998-927-9	Sequence 9, Appli
50	56	67.5	21	5	US-10-484-080-17	Sequence 17, Appl
51	56	67.5	27	4	US-10-361-928-10	Sequence 10, Appl
52	56	67.5	27	4	US-10-157-076-7	Sequence 7, Appli
53	56	67.5	27	4	US-10-157-076-13	Sequence 13, Appl
54	56	67.5	27	5	US-10-959-605-7	Sequence 7, Appli
55	56	67.5	27	5	US-10-959-605-13	Sequence 13, Appl
56	56	67.5	28	3	US-09-843-221A-52	Sequence 52, Appl
57	56	67.5	28	3	US-09-843-221A-168	Sequence 168, App
58	56	67.5	28	3	US-09-999-608-52	Sequence 52, Appl
59	56	67.5	28	4	US-10-157-076-6	Sequence 6, Appli
60	56	67.5	28	4	US-10-157-076-12	Sequence 12, Appl
61	56	67.5	28	4	US-10-839-037-52	Sequence 52, Appl
62	56	67.5	28	4	US-10-839-037-168	Sequence 168, App
63	56	67.5	28	5	US-10-959-605-6	Sequence 6, Appli
64	56	67.5	28	5	US-10-959-605-12	Sequence 12, Appl
65	56	67.5	29	3	US-09-843-221A-51	Sequence 51, Appl
66	56	67.5	29	3	US-09-843-221A-167	Sequence 167, App
67	56	67.5	29	3	US-09-999-608-51	Sequence 51, Appl
68	56	67.5	29	4	US-10-839-037-51	Sequence 51, Appl
69	56	67.5	29	4	US-10-839-037-167	Sequence 167, App
70	56	67.5	30	3	US-09-843-221A-39	Sequence 39, Appl
71	56	67.5	30	3	US-09-843-221A-42	Sequence 42, Appl
72	56	67.5	30	3	US-09-843-221A-47	Sequence 47, Appl
73	56	67.5	30	3	US-09-843-221A-49	Sequence 49, Appl
74	56	67.5	30	3	US-09-843-221A-50	Sequence 50, Appl
75	56	67.5	30	3	US-09-843-221A-124	Sequence 124, App
76	56	67.5	30	3	US-09-843-221A-125	Sequence 125, App
77	56	67.5	30	3	US-09-843-221A-126	Sequence 126, App
78	56	67.5	30	3	US-09-843-221A-127	Sequence 127, App
79	56	67.5	30	3	US-09-843-221A-166	Sequence 166, App
80	56	67.5	30	3	US-09-999-608-39	Sequence 39, Appl
81	56	67.5	30	3	US-09-999-608-42	Sequence 42, Appl
82	56	67.5	30	3	US-09-999-608-47	Sequence 47, Appl
83	56	67.5	30	3	US-09-999-608-49	Sequence 49, Appl
84	56	67.5	30	3	US-09-999-608-50	Sequence 50, Appl
85	56	67.5	30	3	US-09-999-608-124	Sequence 124, App
86	56	67.5	30	3	US-09-999-608-125	Sequence 125, App
87	56	67.5	30	3	US-09-999-608-126	Sequence 126, App
88	56	67.5	30	3	US-09-999-608-127	Sequence 127, App
89	56	67.5	30	3	US-09-999-608-166	Sequence 166, App
90	56	67.5	30	4	US-10-398-449-5	Sequence 5, Appli
91	56	67.5	30	4	US-10-839-037-39	Sequence 39, Appl
92	56	67.5	30	4	US-10-839-037-42	Sequence 42, Appl
93	56	67.5	30	4	US-10-839-037-47	Sequence 47, Appl
94	56	67.5	30	4	US-10-839-037-49	Sequence 49, Appl
95	56	67.5	30	4	US-10-839-037-50	Sequence 50, Appl
96	56	67.5	30	4	US-10-839-037-124	Sequence 124, App
97	56	67.5	30	4	US-10-839-037-125	Sequence 125, App
98	56	67.5	30	4	US-10-839-037-126	Sequence 126, App
99	56	67.5	30	4	US-10-839-037-127	Sequence 127, App
100	56	67.5	30	4	US-10-839-037-166	Sequence 166, App

ALIGNMENTS

RESULT 1
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

Query Match 71.1%; Score 59; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
||||||||||||
Db 1 AVSEIQLMHNLG 12

RESULT 2
US-10-998-927-5
; Sequence 5, Application US/10998927
; Publication No. US20050095236A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, Richard J.
; APPLICANT: Lavigne, Jeffrey R.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid
; TITLE OF INVENTION: Hormone (PTH) 1-84
; FILE REFERENCE: IMUNE-001B
; CURRENT APPLICATION NUMBER: US/10/998,927
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 09/730,174
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates Said Antibodies
US-10-998-927-5

Query Match 71.1%; Score 59; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
||||||||||||
Db 1 AVSEIQLMHNLG 12

RESULT 3
US-09-898-398-3
; Sequence 3, Application US/09898398
; Publication No. US20030082179A1
; GENERAL INFORMATION:
; APPLICANT: Hutchison, James Scott
; TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
; FILE REFERENCE: A1713
; CURRENT APPLICATION NUMBER: US/09/898,398
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-398-3

Query Match 71.1%; Score 59; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
||||||||||||
Db 1 AVSEIQLMHNLG 12

RESULT 4
US-10-921-368-3
; Sequence 3, Application US/10921368
; Publication No. US20050003493A1
; GENERAL INFORMATION:
; APPLICANT: Hutchison, James Scott
; TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
; FILE REFERENCE: A1713
; CURRENT APPLICATION NUMBER: US/10/921,368
; CURRENT FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-368-3

Query Match 71.1%; Score 59; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12
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Db 1 AVSEIQLMHNLG 12

RESULT 5
US-10-192-673-5
; Sequence 5, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT

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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-5

  Query Match             71.1%;  Score 59;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.065;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 6
US-09-730-174A-11
; Sequence 11, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 11
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-11

  Query Match             71.1%;  Score 59;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 7
US-10-998-927-11
; Sequence 11, Application US/10998927
; Publication No. US20050095236A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, Richard J.
;  APPLICANT:  Lavigne, Jeffrey R.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid
;  TITLE OF INVENTION:  Hormone (PTH) 1-84
;  FILE REFERENCE: IMUNE-001B
;  CURRENT APPLICATION NUMBER: US/10/998,927
;  CURRENT FILING DATE:  2004-11-29
;  PRIOR APPLICATION NUMBER: US 09/730,174
;  PRIOR FILING DATE: 2000-12-05
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates Said Antibodies
US-10-998-927-11

  Query Match             71.1%;  Score 59;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 8
US-10-484-080-18
; Sequence 18, Application US/10484080
; Publication No. US20050026839A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  TITLE OF INVENTION: Conformationally Constrained Parathyroid
;  TITLE OF INVENTION:  Hormone (PTH) Analogs
;  FILE REFERENCE: 0609.5110002
;  CURRENT APPLICATION NUMBER: US/10/484,080
;  CURRENT FILING DATE:  2004-01-16
;  PRIOR APPLICATION NUMBER: PCT/US02/22922
;  PRIOR FILING DATE: 2002-07-19
;  PRIOR APPLICATION NUMBER: US 60/326,212
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/306,866
;  PRIOR FILING DATE: 2001-07-23
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-484-080-18

  Query Match             71.1%;  Score 59;  DB 5;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.097;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 9
US-10-361-928-7
; Sequence 7, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
;  APPLICANT: BRINGHURST, F. RICHARD
;  APPLICANT:  TAKASU, HISASHI
;  APPLICANT:  GARDELLA, THOMAS J.
;  TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
;  TITLE OF INVENTION:  ANALOGS
;  FILE REFERENCE: 0609.4630002
;  CURRENT APPLICATION NUMBER: US/10/361,928
;  CURRENT FILING DATE:  2003-02-11
;  PRIOR APPLICATION NUMBER: 09/447,800
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: 60/110,152
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ala
US-10-361-928-7

  Query Match             71.1%;  Score 59;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
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              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 10
US-10-157-076-5
; Sequence 5, Application US/10157076
; Publication No. US20040176568A1
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/157,076
;  CURRENT FILING DATE:  2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-157-076-5

  Query Match             71.1%;  Score 59;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 11
US-10-157-076-9
; Sequence 9, Application US/10157076
; Publication No. US20040176568A1
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/157,076
;  CURRENT FILING DATE:  2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-157-076-9

  Query Match             71.1%;  Score 59;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 12
US-10-959-605-5
; Sequence 5, Application US/10959605
; Publication No. US20050203012A1
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
;  TITLE OF INVENTION:  and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/959,605
;  CURRENT FILING DATE:  2004-10-07
;  PRIOR APPLICATION NUMBER: US/10/157,076
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-959-605-5

  Query Match             71.1%;  Score 59;  DB 5;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
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Db          1 AVSEIQLMHNLG 12


RESULT 13
US-10-959-605-9
; Sequence 9, Application US/10959605
; Publication No. US20050203012A1
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
;  TITLE OF INVENTION:  and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/959,605
;  CURRENT FILING DATE:  2004-10-07
;  PRIOR APPLICATION NUMBER: US/10/157,076
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-959-605-9

  Query Match             71.1%;  Score 59;  DB 5;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
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Db          1 AVSEIQLMHNLG 12
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RESULT 14
US-10-157-076-4
; Sequence 4, Application US/10157076
; Publication No. US20040176568A1
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/157,076
;  CURRENT FILING DATE:  2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-157-076-4

  Query Match             71.1%;  Score 59;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 15
US-10-157-076-8
; Sequence 8, Application US/10157076
; Publication No. US20040176568A1
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/157,076
;  CURRENT FILING DATE:  2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-157-076-8

  Query Match             71.1%;  Score 59;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 16
US-10-959-605-4
; Sequence 4, Application US/10959605
; Publication No. US20050203012A1
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
;  TITLE OF INVENTION:  and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/959,605
;  CURRENT FILING DATE:  2004-10-07
;  PRIOR APPLICATION NUMBER: US/10/157,076
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-959-605-4

  Query Match             71.1%;  Score 59;  DB 5;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
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Db          1 AVSEIQLMHNLG 12


RESULT 17
US-10-959-605-8
; Sequence 8, Application US/10959605
; Publication No. US20050203012A1
; GENERAL INFORMATION:
;  APPLICANT: Bringhurst, F. Richard
;  APPLICANT:  Takasu, Hisashi
;  APPLICANT:  Gardella, Thomas J.
;  APPLICANT:  Potts, John T. Jr.
;  TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
;  TITLE OF INVENTION:  and Use
;  FILE REFERENCE: 0609.4640002
;  CURRENT APPLICATION NUMBER: US/10/959,605
;  CURRENT FILING DATE:  2004-10-07
;  PRIOR APPLICATION NUMBER: US/10/157,076
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: US 09/448,867
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: US 60/109,938
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-959-605-8

  Query Match             71.1%;  Score 59;  DB 5;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
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Db          1 AVSEIQLMHNLG 12


RESULT 18
US-09-843-221A-48
; Sequence 48, Application US/09843221A
; Publication No. US20030039654A1
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; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/09/843,221A
;  CURRENT FILING DATE:  2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: rat PTH
US-09-843-221A-48

  Query Match             71.1%;  Score 59;  DB 3;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 19
US-09-999-608-48
; Sequence 48, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  GEGG, COLIN V.
;  APPLICANT:  JAROSINSKI, MARK ANTHONY
;  APPLICANT:  KINSTLER, OLAF BORIS
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
;  TITLE OF INVENTION:  HORMONE-RELATED PROTEIN
;  FILE REFERENCE: A-665C
;  CURRENT APPLICATION NUMBER: US/09/999,608
;  CURRENT FILING DATE:  2002-03-11
;  PRIOR APPLICATION NUMBER: US 09/843,221
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: US 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: US 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 193
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: rat PTH
US-09-999-608-48

  Query Match             71.1%;  Score 59;  DB 3;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 20
US-10-839-037-48
; Sequence 48, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTENUIK, PAUL
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  LACEY, DAVID LEE
;  TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HO
;  TITLE OF INVENTION:  RELATED PROTEIN
;  FILE REFERENCE: A-665B
;  CURRENT APPLICATION NUMBER: US/10/839,037
;  CURRENT FILING DATE:  2004-05-04
;  PRIOR APPLICATION NUMBER: US/09/843,221A
;  PRIOR FILING DATE: 2001-04-26
;  PRIOR APPLICATION NUMBER: 60/266,673
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/214,860
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/200,053
;  PRIOR FILING DATE: 2000-04-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: rat PTH
US-10-839-037-48

  Query Match             71.1%;  Score 59;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
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Db          1 AVSEIQLMHNLG 12


Search completed: November 21, 2005, 16:56:22
Job time : 164 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 21, 2005, 16:43:05 ; Search time 6 Seconds
(without alignments)
3.013 Million cell updates/sec

Title: SEQ-NEW
Perfect score: 83
Sequence: 1 avseiqlmhnlggggg 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	56.6	28	1	US-10-939-890-464	Sequence 464, App
2	47	56.6	28	1	US-10-939-890-720	Sequence 720, App
3	47	56.6	28	1	US-10-939-890-723	Sequence 723, App
4	44	53.0	28	1	US-10-939-890-353	Sequence 353, App
5	44	53.0	28	1	US-10-939-890-829	Sequence 829, App
6	42	50.6	27	1	US-10-939-890-354	Sequence 354, App
7	42	50.6	27	1	US-10-939-890-830	Sequence 830, App
8	38	45.8	28	1	US-10-939-890-346	Sequence 346, App
9	38	45.8	28	1	US-10-939-890-383	Sequence 383, App
10	38	45.8	28	1	US-10-939-890-699	Sequence 699, App
11	38	45.8	28	1	US-10-939-890-822	Sequence 822, App
12	37.5	45.2	114	1	US-10-972-587-37	Sequence 37, Appl
13	37	44.6	27	1	US-10-939-890-700	Sequence 700, App
14	37	44.6	28	1	US-10-939-890-384	Sequence 384, App
15	37	44.6	368	1	US-10-689-742-100	Sequence 100, App
16	35	42.2	431	7	US-11-169-013-2	Sequence 2, Appli
17	35	42.2	2047	7	US-11-013-759-4	Sequence 4, Appli
18	35	42.2	2047	7	US-11-013-759-7	Sequence 7, Appli
19	35	42.2	2053	7	US-11-013-759-9	Sequence 9, Appli
20	34	41.0	28	1	US-10-939-890-325	Sequence 325, App
21	34	41.0	28	1	US-10-939-890-351	Sequence 351, App
22	34	41.0	28	1	US-10-939-890-827	Sequence 827, App
23	34	41.0	29	1	US-10-939-890-350	Sequence 350, App
24	34	41.0	29	1	US-10-939-890-381	Sequence 381, App
25	34	41.0	29	1	US-10-939-890-697	Sequence 697, App
26	34	41.0	29	1	US-10-939-890-826	Sequence 826, App
27	34	41.0	255	1	US-10-660-499A-2	Sequence 2, Appli
28	33.5	40.4	148	1	US-10-526-716-2	Sequence 2, Appli
29	33	39.8	27	1	US-10-939-890-751	Sequence 751, App
30	33	39.8	27	1	US-10-939-890-752	Sequence 752, App
31	33	39.8	27	1	US-10-939-890-762	Sequence 762, App
32	33	39.8	28	1	US-10-939-890-356	Sequence 356, App
33	33	39.8	28	1	US-10-939-890-630	Sequence 630, App
34	33	39.8	28	1	US-10-939-890-719	Sequence 719, App
35	33	39.8	28	1	US-10-939-890-721	Sequence 721, App
36	33	39.8	28	1	US-10-939-890-722	Sequence 722, App
37	33	39.8	28	1	US-10-939-890-794	Sequence 794, App
38	33	39.8	28	1	US-10-939-890-795	Sequence 795, App
39	33	39.8	28	1	US-10-939-890-832	Sequence 832, App
40	33	39.8	28	1	US-10-939-890-847	Sequence 847, App
41	33	39.8	29	1	US-10-939-890-495	Sequence 495, App
42	33	39.8	29	1	US-10-939-890-629	Sequence 629, App
43	33	39.8	29	1	US-10-939-890-640	Sequence 640, App
44	33	39.8	29	1	US-10-939-890-848	Sequence 848, App
45	33	39.8	29	1	US-10-939-890-854	Sequence 854, App
46	33	39.8	148	1	US-10-526-716-4	Sequence 4, Appli
47	33	39.8	157	1	US-10-957-569-64	Sequence 64, Appl
48	33	39.8	745	1	US-10-131-826A-68	Sequence 68, Appl
49	32.5	39.2	579	1	US-10-975-798-4	Sequence 4, Appli
50	32.5	39.2	580	1	US-10-975-798-3	Sequence 3, Appli
51	32	38.6	628	7	US-11-074-176-244	Sequence 244, App
52	31.5	38.0	605	1	US-10-131-826A-160	Sequence 160, App
53	31	37.3	27	1	US-10-939-890-343	Sequence 343, App
54	31	37.3	27	1	US-10-939-890-819	Sequence 819, App
55	31	37.3	28	1	US-10-939-890-355	Sequence 355, App
56	31	37.3	28	1	US-10-939-890-474	Sequence 474, App
57	31	37.3	28	1	US-10-939-890-726	Sequence 726, App
58	31	37.3	28	1	US-10-939-890-831	Sequence 831, App
59	31	37.3	239	1	US-10-957-569-54	Sequence 54, Appl
60	31	37.3	396	1	US-10-510-386-238	Sequence 238, App
61	31	37.3	399	1	US-10-510-386-30	Sequence 30, Appl
62	31	37.3	420	7	US-11-074-176-48	Sequence 48, Appl
63	31	37.3	497	1	US-10-984-376-3	Sequence 3, Appli
64	31	37.3	825	7	US-11-074-176-20	Sequence 20, Appl
65	30	36.1	6	7	US-11-057-058-3	Sequence 3, Appli
66	30	36.1	22	1	US-10-939-890-267	Sequence 267, App
67	30	36.1	26	1	US-10-939-890-380	Sequence 380, App
68	30	36.1	26	1	US-10-939-890-696	Sequence 696, App
69	30	36.1	27	1	US-10-939-890-319	Sequence 319, App
70	30	36.1	27	1	US-10-939-890-340	Sequence 340, App
71	30	36.1	27	1	US-10-939-890-341	Sequence 341, App
72	30	36.1	27	1	US-10-939-890-342	Sequence 342, App
73	30	36.1	27	1	US-10-939-890-352	Sequence 352, App
74	30	36.1	27	1	US-10-939-890-816	Sequence 816, App
75	30	36.1	27	1	US-10-939-890-817	Sequence 817, App
76	30	36.1	27	1	US-10-939-890-818	Sequence 818, App
77	30	36.1	27	1	US-10-939-890-828	Sequence 828, App
78	30	36.1	28	1	US-10-939-890-326	Sequence 326, App
79	30	36.1	28	1	US-10-939-890-344	Sequence 344, App
80	30	36.1	28	1	US-10-939-890-345	Sequence 345, App
81	30	36.1	28	1	US-10-939-890-382	Sequence 382, App
82	30	36.1	28	1	US-10-939-890-385	Sequence 385, App
83	30	36.1	28	1	US-10-939-890-698	Sequence 698, App
84	30	36.1	28	1	US-10-939-890-701	Sequence 701, App
85	30	36.1	28	1	US-10-939-890-820	Sequence 820, App
86	30	36.1	28	1	US-10-939-890-821	Sequence 821, App
87	30	36.1	158	1	US-10-467-962B-83	Sequence 83, Appl
88	30	36.1	167	1	US-10-967-457-79	Sequence 79, Appl
89	30	36.1	200	1	US-10-841-129-7	Sequence 7, Appli
90	30	36.1	200	7	US-11-060-659-32	Sequence 32, Appl
91	30	36.1	263	7	US-11-040-638-2	Sequence 2, Appli
92	30	36.1	269	1	US-10-131-826A-532	Sequence 532, App
93	30	36.1	318	1	US-10-802-796-727	Sequence 727, App
94	30	36.1	334	1	US-10-802-796-728	Sequence 728, App
95	30	36.1	371	1	US-10-512-184-71	Sequence 71, Appl
96	30	36.1	379	7	US-11-109-156-16	Sequence 16, Appl
97	30	36.1	386	1	US-10-131-826A-340	Sequence 340, App
98	30	36.1	429	1	US-10-984-376-2	Sequence 2, Appli

99	30	36.1	465	1	US-10-967-648A-6	Sequence 6, Appli
100	30	36.1	467	7	US-11-082-389-334	Sequence 334, App

ALIGNMENTS

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RESULT 1
US-10-939-890-464
; Sequence 464, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 464
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Library Isolate
US-10-939-890-464

  Query Match             56.6%;  Score 47;  DB 1;  Length 28;
  Best Local Similarity   57.1%;  Pred. No. 0.02;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 SEIQLMHNLGGGGG 16
              :::|| |  |||||
Db         14 ADLQLSHFAGGGGG 27


RESULT 2
US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 720
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: ACETYLATION
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-720

  Query Match             56.6%;  Score 47;  DB 1;  Length 28;
  Best Local Similarity   57.1%;  Pred. No. 0.02;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 SEIQLMHNLGGGGG 16
              :::|| |  |||||
Db         14 ADLQLSHFAGGGGG 27


RESULT 3
US-10-939-890-723
; Sequence 723, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
```

```
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 723
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: ACETYLATION
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: Lys residue modifed with a SATA linker
US-10-939-890-723

  Query Match             56.6%;  Score 47;  DB 1;  Length 28;
  Best Local Similarity   57.1%;  Pred. No. 0.02;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 SEIQLMHNLGGGGG 16
              :::|| |  |||||
Db         14 ADLQLSHFAGGGGG 27


RESULT 4
US-10-939-890-353
; Sequence 353, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 353
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-353

  Query Match             53.0%;  Score 44;  DB 1;  Length 28;
  Best Local Similarity   70.0%;  Pred. No. 0.057;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 LMHNLGGGGG 16
              : | ||||||
Db         18 MFHQLGGGGG 27


RESULT 5
US-10-939-890-829
; Sequence 829, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 829
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;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: ACETYLATION
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-829

  Query Match             53.0%;  Score 44;  DB 1;  Length 28;
  Best Local Similarity   70.0%;  Pred. No. 0.057;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 LMHNLGGGGG 16
              : | ||||||
Db         18 MFHQLGGGGG 27


RESULT 6
US-10-939-890-354
; Sequence 354, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 354
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-354

  Query Match             50.6%;  Score 42;  DB 1;  Length 27;
  Best Local Similarity   53.8%;  Pred. No. 0.11;
  Matches    7;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 EIQLMHNLGGGGG 16
              |::|: : |||||
Db         14 EVELVDHPGGGGG 26


RESULT 7
US-10-939-890-830
; Sequence 830, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 830
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: ACETYLATION
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (27)..(27)
;   OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-830

  Query Match             50.6%;  Score 42;  DB 1;  Length 27;
  Best Local Similarity   53.8%;  Pred. No. 0.11;
  Matches    7;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 EIQLMHNLGGGGG 16
              |::|: : |||||
Db         14 EVELVDHPGGGGG 26
```

```
RESULT 8
US-10-939-890-346
; Sequence 346, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 346
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-346

  Query Match             45.8%;  Score 38;  DB 1;  Length 28;
  Best Local Similarity   70.0%;  Pred. No. 0.48;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 LMHNLGGGGG 16
              | |: |||||
Db         18 LNHSPGGGGG 27


RESULT 9
US-10-939-890-383
; Sequence 383, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 383
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Library Isolate
US-10-939-890-383

  Query Match             45.8%;  Score 38;  DB 1;  Length 28;
  Best Local Similarity   70.0%;  Pred. No. 0.48;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 LMHNLGGGGG 16
              | |: |||||
Db         18 LNHSPGGGGG 27


RESULT 10
US-10-939-890-699
; Sequence 699, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
```

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;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 699
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: ACETYLATION
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-699

  Query Match             45.8%;  Score 38;  DB 1;  Length 28;
  Best Local Similarity   70.0%;  Pred. No. 0.48;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 LMHNLGGGGG 16
              | |: |||||
Db         18 LNHSPGGGGG 27


RESULT 11
US-10-939-890-822
; Sequence 822, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
;  APPLICANT:  Khurana, Sudha
;  APPLICANT:  Linder, Karen E.
;  APPLICANT:  Marinelli, Edmund R.
;  APPLICANT:  Nanjappan, Palaniappa
;  APPLICANT:  Nunn, Adrian D.
;  APPLICANT:  Pillai, Radhakrishna
;  APPLICANT:  Pochon, Sibylle
;  APPLICANT:  Ramalingam, Kondareddiar
;  APPLICANT:  Shrivastava, Ajay
;  APPLICANT:  Song, Bo
;  APPLICANT:  Swenson, Rolf E.
;  APPLICANT:  Von Wronski, Mathew A.
;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: PCT/US03/06731
;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 822
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: ACETYLATION
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (9)..(9)
;   OTHER INFORMATION: Lys residue modified with a iv-Dde linker
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-822

  Query Match             45.8%;  Score 38;  DB 1;  Length 28;
  Best Local Similarity   70.0%;  Pred. No. 0.48;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 LMHNLGGGGG 16
              | |: |||||
Db         18 LNHSPGGGGG 27


RESULT 12
US-10-972-587-37
; Sequence 37, Application US/10972587
; Publication No. US20050246799A1
; GENERAL INFORMATION:
;  APPLICANT: Song, Xiaoling
;  APPLICANT:  Bariola, Pauline Anne
;  APPLICANT:  Linderoth, Nora Abiella
;  APPLICANT:  Fan, Hao
;  APPLICANT:  Wei, Zhong-Min
;  TITLE OF INVENTION: RECEPTORS FOR HYPERSENSITIVE RESPONSE ELICITORS AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: 21829/213
;  CURRENT APPLICATION NUMBER: US/10/972,587
;  CURRENT FILING DATE:  2004-10-25
;  PRIOR APPLICATION NUMBER: 60/335,776
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 09/810,997
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 10/174,209
;  PRIOR FILING DATE: 2002-06-17
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Xanthomonas campestris pv. pelargonii
US-10-972-587-37

  Query Match             45.2%;  Score 37.5;  DB 1;  Length 114;
  Best Local Similarity   60.0%;  Pred. No. 2.4;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          5 IQLMHNLGG---GGG 16
              :||| | ||   |||
Db         89 MQLMQNQGGAGMGGG 103


RESULT 13
US-10-939-890-700
; Sequence 700, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
```

; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 700
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (27)..(27)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-700

Query Match 44.6%; Score 37; DB 1; Length 27;
Best Local Similarity 85.7%; Pred. No. 0.65;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGGGGG 16
|:|||||
Db 20 NVGGGGG 26

RESULT 14
US-10-939-890-384
; Sequence 384, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 384
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-384

Query Match 44.6%; Score 37; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 0.68;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGGGGG 16
|:|||||
Db 21 NVGGGGG 27

RESULT 15
US-10-689-742-100
; Sequence 100, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 100
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-100

Query Match 44.6%; Score 37; DB 1; Length 368;
Best Local Similarity 53.8%; Pred. No. 9.7;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 VSEIQLMHNLGGG 14
              |: :| | | |||
Db         59 VNSLQKMQNKGGG 71


RESULT 16
US-11-169-013-2
; Sequence 2, Application US/11169013
; Publication No. US20050244971A1
; GENERAL INFORMATION:
;  APPLICANT: Korea Kumho Petrochemical Co., Ltd.
;  TITLE OF INVENTION: TRANSGENIC PLANTS WITH ENHANCED STRESS TOLERANCE
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/169,013
;  CURRENT FILING DATE:  2005-06-29
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 2
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-11-169-013-2

  Query Match             42.2%;  Score 35;  DB 7;  Length 431;
  Best Local Similarity   85.7%;  Pred. No. 23;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNLGGGG 15
              :||||||
Db          8 NNLGGGG 14


RESULT 17
US-11-013-759-4
; Sequence 4, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
;  APPLICANT: Loosmore, Sheena M.
;  APPLICANT:  Sasaki, Ken
;  APPLICANT:  Yang, Yan Ping
;  APPLICANT:  Klein, Michel H.
;  TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
;  TITLE OF INVENTION:  PROTEIN OF MORAXELLA
;  FILE REFERENCE: 1038-921MIS:jb
;  CURRENT APPLICATION NUMBER: US/11/013,759
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: US/09/361,619
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2047
;   TYPE: PRT
;   ORGANISM: Moraxella catarrhalis
US-11-013-759-4

  Query Match             42.2%;  Score 35;  DB 7;  Length 2047;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGG 14
              ||:|    |: |||
Db         18 AVAEYAKSHSTGGG 31


RESULT 18
US-11-013-759-7
; Sequence 7, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
;  APPLICANT: Loosmore, Sheena M.
;  APPLICANT:  Sasaki, Ken
;  APPLICANT:  Yang, Yan Ping
;  APPLICANT:  Klein, Michel H.
;  TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
;  TITLE OF INVENTION:  PROTEIN OF MORAXELLA
;  FILE REFERENCE: 1038-921MIS:jb
;  CURRENT APPLICATION NUMBER: US/11/013,759
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: US/09/361,619
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 2047
;   TYPE: PRT
;   ORGANISM: Moraxella catarrhalis
US-11-013-759-7

  Query Match             42.2%;  Score 35;  DB 7;  Length 2047;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGG 14
              ||:|    |: |||
Db         18 AVAEYAKSHSTGGG 31


RESULT 19
US-11-013-759-9
; Sequence 9, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
;  APPLICANT: Loosmore, Sheena M.
;  APPLICANT:  Sasaki, Ken
;  APPLICANT:  Yang, Yan Ping
;  APPLICANT:  Klein, Michel H.
;  TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
;  TITLE OF INVENTION:  PROTEIN OF MORAXELLA
;  FILE REFERENCE: 1038-921MIS:jb
;  CURRENT APPLICATION NUMBER: US/11/013,759
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: US/09/361,619
;  PRIOR FILING DATE: 1999-07-27
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 2053
;   TYPE: PRT
;   ORGANISM: Moraxella catarrhalis
US-11-013-759-9

  Query Match             42.2%;  Score 35;  DB 7;  Length 2053;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLGGG 14
              ||:|    |: |||
Db         18 AVAEYAKSHSTGGG 31


RESULT 20
US-10-939-890-325
; Sequence 325, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Sexton, Daniel J.
;  APPLICANT:  Dransfield, Daniel T.
;  APPLICANT:  Ladner, Robert C.
;  APPLICANT:  Arbogast, Christophe
;  APPLICANT:  Bussat, Philippe
;  APPLICANT:  Fan, Hong
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;  TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;  FILE REFERENCE: D0617.70014US00
;  CURRENT APPLICATION NUMBER: US/10/939,890
;  CURRENT FILING DATE:  2004-09-13
;  PRIOR APPLICATION NUMBER: US 10/661,156
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: US 10/382,082
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;  PRIOR FILING DATE: 2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/440,411
;  PRIOR FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: US 60/360,851
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 883
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 325
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-325

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  Best Local Similarity   58.3%;  Pred. No. 2;
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              || : :| ||||
Db         15 IQRVDSLTGGGG 26


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